

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:16:57 ; Search time 8599.76 Seconds  
(without alignments)  
11720.367 Million cell

updates/sec

Title: US-10-054-680-1  
Perfect score: 2766  
Sequence: 1 atggcgtgggtaagggttgca.....gctacatcaaggggttctaa  
2766

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
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1	2627.4	95.0	3186	3	BC036783	BC036783 Homo	
sapi							
2	1786.4	64.6	1788	9	AY401283	AY401283 Homo	
sapi							
3	1741.4	63.0	1788	9	AY401284	AY401284 Pan	
trogl							

4	1624.4	58.7	2534	3	AK044636	AK044636 Mus
muscu						
5	1546.4	55.9	1788	9	AY401285	AY401285 Mus
muscu						
6	1258.2	45.5	4374	3	AK035163	AK035163 Mus
muscu						
7	1208.8	43.7	2922	9	AY398961	AY398961 Homo
sapi						
8	1169.8	42.3	2922	9	AY398963	AY398963 Mus
muscu						
9	1151.4	41.6	2516	9	AY408693	AY408693 Homo
sapi						
10	978.4	35.4	2881	9	AY398962	AY398962 Pan
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12	948.4	34.3	3573	3	AK048160	AK048160 Mus
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13	899.2	32.5	938	5	BX374548	BX374548
BX374548						
14	874.8	31.6	2515	9	AY408695	AY408695 Mus
muscu						
15	813.8	29.4	887	4	BI913344	BI913344
603178823						
16	768.2	27.8	939	5	BX347210	BX347210
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c 17	743.4	26.9	791	4	BI523145	BI523145
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19	737.8	26.7	916	5	BX368185	BX368185
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21	698.2	25.2	2472	9	AY408694	AY408694 Pan
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22	673.2	24.3	775	5	BQ770745	BQ770745 UI-
M-FI0-						
23	657	23.8	665	5	BQ189572	BQ189572 UI-
E-EJ1-						
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M-HD0-						
25	598.6	21.6	944	5	BX368184	BX368184
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muscu						
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M-GH0-						
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Tetraodon						
30	516	18.7	527	4	BG910325	BG910325
602805921						
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M-FY0-						
32	483.2	17.5	851	5	BX325851	BX325851
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34	452	16.3	717	5	BX501230	BX501230
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36	422.8	15.3	684	5	BU363818	BU363818
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#### ALIGNMENTS

RESULT 1  
BC036783  
LOCUS BC036783 3186 bp mRNA linear HTC 19-  
NOV-2003  
DEFINITION Homo sapiens solute carrier family 8 (sodium-calcium  
exchanger),  
member 3, mRNA (cDNA clone IMAGE:5732743), with apparent  
retained  
intron.  
ACCESSION BC036783  
VERSION BC036783.1 GI:23331089  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3186)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M.,  
Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F.,  
Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.,  
Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M.,  
Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A.,  
Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X.,  
 Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J.,  
 Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-  
 length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 MEDLINE 22388257  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 3186)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-AUG-2002) National Institutes of Health,  
 Mammalian Gene Collection (MGC), Cancer Genomics Office, National  
 Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-  
 2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,  
 Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P.,  
 Legaspi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B.,  
 Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J.,  
 Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D.,  
 Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.  
 Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Series: IRAK Plate: 79 Row: j Column: 21  
 This clone was selected for full length sequencing because  
 it



passed the following selection criteria: matched mRNA gi:  
17865803

This clone has the following problem: retained intron.

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/clone="IMAGE:5732743"  
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/clone\_lib="NIH MGC\_124"  
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/note="Vector: pCMV-SPORT6"

ORIGIN

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Matches 2628; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;

Qy 1  
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Qy 61  
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Qy 121  
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Qy 181  
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Qy 481  
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Qy 721  
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Qy 841  
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Qy 901  
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Qy 1081  
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Qy 1201  
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RESULT 2

AY401283

LOCUS AY401283 1788 bp DNA linear GSS 15-

DEC-2003

DEFINITION Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial  
sequence,

genomic survey sequence.

ACCESSION AY401283

VERSION AY401283.1 GI:39757272

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse  
orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and  
ordering them based on alignment.

FEATURES Location/Qualifiers  
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ORIGIN

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Gaps 0;

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Qy 661  
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Qy 1021  
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RESULT 3

AY401284

LOCUS AY401284 1788 bp DNA linear GSS 15-

DEC-2003

DEFINITION Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial  
sequence,

genomic survey sequence.

ACCESSION AY401284

VERSION AY401284.1 GI:39757273

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1 (bases 1 to 1788)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse  
orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1788)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and  
ordering  
them based on alignment.  
FEATURES Location/Qualifiers  
source 1. .1788  
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Qy 361  
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Qy 661  
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|||||
Db          721
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Db          901
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Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788  
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# RESULT 4

AK044636

LOCUS AK044636 2534 bp mRNA linear HTC 03-

APR-2004

DEFINITION Mus musculus adult retina cDNA, RIKEN full-length enriched library,

clone:A930029A02 product:solute carrier family 8 (sodium/calcium

exchanger), member 3, full insert sequence....

ACCESSION AK044636

VERSION AK044636.1 GI:26336660

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y.,  
Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and

Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of

new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N.,  
Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H.,  
Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,  
Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,  
Kashiwagi,K.,

Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M.,

Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S.,  
Kawai,J.,

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team  
and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration  
Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional  
annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 2534)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H.,  
Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T.,  
Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I.,  
Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M.,  
Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K.,  
Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-  
Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute  
of Physical and Chemical Research (RIKEN), Laboratory for  
Genome Exploration Research Group, RIKEN Genomic Sciences Center  
(GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,  
Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in  
Riken Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues.  
Retina RNA was provided by Dr. Stefano Gustincich  
(Department of Neurobiology, Harvard Medical School, 220 Longwood Ave.,



Boston, MA 02115, USA) whose assistance is gratefully acknowledged.

Please visit our web site for further details.  
 URL: <http://genome.gsc.riken.jp/>  
 URL: <http://fantom.gsc.riken.jp/>.

FEATURES  
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 ORIGIN

Query Match 58.7%; Score 1624.4; DB 3; Length 2534;  
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Db 783  
 GCCAACTCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCT 842

Qy 239  
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Db 843  
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Qy 359  
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Qy 539

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Qy 1019  
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Db      2223
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Qy      1679
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Db      2283
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Qy      1739
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Db      2343
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Qy      1799
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Db      2403
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RESULT 5

AY401285

LOCUS AY401285 1788 bp DNA linear GSS 15-  
DEC-2003

DEFINITION Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial  
sequence,

genomic survey sequence.

ACCESSION AY401285

VERSION AY401285.1 GI:39757274

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
Murinae; Mus.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse  
 orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1788)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
 Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and  
 ordering them based on alignment.  
 FEATURES Location/Qualifiers  
 source 1. .1788  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 gene <1..>1788  
 /gene="SLC8A3"  
 /locus\_tag="HCM0839"  
 ORIGIN

Query Match 55.9%; Score 1546.4; DB 9; Length 1788;  
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 Gaps 0;

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Qy          61
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Db          61
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Db          121
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Db 301  
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Qy 361  
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Db 361  
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Qy 481  
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Db 661  
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Db 781  
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Db 841  
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Db 901  
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Db 961  
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Qy 1021  
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Db 1021  
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Qy 1081  
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Qy 1381  
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Db 1381  
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RESULT 6  
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 APR-2004  
 DEFINITION Mus musculus 12 days embryo embryonic body between diaphragm  
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 clone:9430095C22  
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 ACCESSION AK035163  
 VERSION AK035163.1 GI:26084435  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
 Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y.,  
 Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and  
 Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs  
 to  
 prepare full-length cDNA libraries for rapid discovery of  
 new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N.,  
 Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H.,  
 Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,  
 Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,  
 Kashiwagi,K.,  
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watahiki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S.,  
 Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
 Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4

AUTHORS and the The RIKEN Genome Exploration Research Group Phase II Team  
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration  
Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional  
annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4374)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H.,  
Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T.,  
Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I.,  
Kasukawa,T.,  
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M.,  
Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K.,  
Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-  
Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute  
of  
Physical and Chemical Research (RIKEN), Laboratory for  
Genome  
Exploration Research Group, RIKEN Genomic Sciences Center  
(GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,  
Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in  
Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN.  
Division of Experimental Animal Research in Riken  
contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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# ORIGIN

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Qy 556
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Qy 676
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CCG 1417

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Qy 1264  
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Qy 1504  
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Db 1943  
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Qy 1966  
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Qy 2026  
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Qy 2203  
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REFERENCE      2   (bases 1 to 2922)
AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,
Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and
ordering       them based on alignment.
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    gene              <1..>2922
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                        /locus_tag="HCM0065"
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Best Local Similarity 66.9%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 762; Indels 171;
Gaps 5;

Qy               109
GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTTCAAGGGTCATCGGACTGCAAGGAG 168
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Qy               169
GGTGTCATCCTGCCAATCTGGTACCCGGGAGAACCCCTTCCCTTGGGGACAAGATTGCCAGG 228
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Db               172
GGGGTGATTTTGCCCATTGTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 231
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Qy               229
GTCATTGTCTATTTTGTGGCCCTGATATAACATGTTTCCCTTGGGGGTGTCCATCATTGCTGAC 288
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Db               232
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Qy               289
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|||||
Db               292
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Qy               349
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Db               352

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CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 411  
 Qy 409  
 ACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468  
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 Db 412  
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 Db 472  
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Qy 922  
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Db 952  
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Db 1132  
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Qy 1162 ACCGATGAGCCTG---  
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Qy 1219  
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Db 1312  
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Qy 1339  
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Qy          1399  
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Qy          1459  
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Db          1492 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----  
CAATCAT 1542  
  
Qy          1519  
CCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGATGAT 1578  
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Qy          1639  
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Qy          1699  
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Db          1723  
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Qy          1759  
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Db          1783  
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Qy          1819  
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Qy          1876  
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Qy 1876 ----- 1875

Db 1963  
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Db 2143  
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Qy 2047  
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Qy 2107  
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GACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCC 2226  
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Db 2323  
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Qy 2227  
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Db 2383  
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Qy 2287  
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Db 2503  
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Qy 2467  
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TGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTCTAA 2766  
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Db 2863  
TGGCTCTTGACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAAGGCTTCTAA 2922

RESULT 8  
AY398963  
LOCUS AY398963 2922 bp DNA linear GSS 15-  
DEC-2003  
DEFINITION Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial  
sequence,  
genomic survey sequence.

ACCESSION AY398963  
 VERSION AY398963.1 GI:39754952  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
 Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2922)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
 Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse  
 orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2922)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
 Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and  
 ordering  
 them based on alignment.  
 FEATURES Location/Qualifiers  
 source 1. .2922  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 gene <1..>2922  
 /gene="SLC8A1"  
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# ORIGIN

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 Best Local Similarity 66.2%; Pred. No. 5.4e-313;  
 Matches 1845; Conservative 0; Mismatches 771; Indels 171;  
 Gaps 5;

Qy 142  
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 Db 145  
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 Qy 202  
 CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG 261  
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Qy 262  
TTCCTTGGGGTGTCATCATTTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT 321  
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Db 265  
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Qy 322  
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Db 325  
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Qy 382  
GTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCCCTGGGTTCTCTGCTCCTGAG 441  
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Db 385  
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Qy 442  
ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTATTGCTGGTGATCTGGGACCT 501  
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Db 445  
ATTCTCCTGTGAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC 504

Qy 502  
TCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTAC 561  
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Db 505  
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Qy 562  
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Db 565  
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Qy 622  
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Db 625  
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Qy 682  
GTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTG 741  
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Db 685  
GTTGTGGAGGTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTTCCCATCTGCGTTGTGTTC 744

Qy 742  
GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACA 801  
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Db 745  
GCGTGGGTAGCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCC 804

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TAAGGGC 852  
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Db 805  
GGCAAGCAGAGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAACTGAA 864

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Db 865  
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Qy 913 GAAGGG-----  
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Db 925  
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Qy 955  
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Db 985  
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Qy 1015  
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Qy 1075  
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Db 1105  
ACTCGCCTGATGACCGGAGCTGGCAACATCTTGAAGAGGCACGCAGCTGATCAAGCAAGG 1164

Qy 1135 AAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTG---  
AGGACTTTATTTCCAAG 1191  
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Db 1165  
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Qy 1192  
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Db 1225  
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Qy 1252

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 Db 1405  
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Db 1876  
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Qy 1906  
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Qy 1906  
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Db 1996  
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Db 2056  
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Db 2116  
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Qy 2020  
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 Db 2776  
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RESULT 9

AY408693

LOCUS AY408693 2516 bp DNA linear GSS 12-

DEC-2003

DEFINITION Homo sapiens HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY408693

VERSION AY408693.1 GI:39764664

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2516)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
 Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse  
 orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2516)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
 Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and  
 ordering

them based on alignment.

FEATURES Location/Qualifiers

source

1. .2516

/organism="Homo sapiens"

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/db\_xref="taxon:9606"

gene

<1..>2516

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ORIGIN

Query Match 41.6%; Score 1151.4; DB 9; Length 2516;  
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Qy 266

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AGAGGGAGGTGACAATTAAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCCGGGTCT 385

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Qy 386  
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|  
Db 121  
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Qy 446  
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Qy 506  
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Db 241  
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Qy 566  
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Qy 626  
GGAGTATCTTTGCCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCCTGGTGTGG 685

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Db 361  
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Db 421  
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Db 481  
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Db 541  
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CCTGGTGCCCCCTGG 913  
|  
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Db 781  
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Qy 1094  
CAGGCAATATCCTGAAGAAACATGCAGCAGAAACAAGCCAAGAAGGCCTCCAGCATGAGCG 1153  
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Db 841 CCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGGGCGGC---  
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Qy 1214  
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Db 958  
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Qy 1274  
TGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTG 1333  
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Db 1018



GCAACAGCACCTTCTACGTGGACTACCGCACTGAGGACGGCTCTGCCAAGGCGGGCTCCG 1077

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Db          1543
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Qy          1874 AACGTGGAATATCAGATGTGACA-----
GACAGGAAGCTGACTATGG 1915
      | || || || |||
|
Db          1603
AGCGAGGGATTTCAGNNNNNNNNNNNNNNNNNNNGGGATGGGGACAGGAAGCTAACAGCCG 1662

Qy          1916
AAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCA 1975
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Db          1663
AGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTTCTTGGGGAGAACTGCC 1722

Qy          1976
AACTAGAAGTCATCATTTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCA 2035
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Qy          2036
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Db          1783
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Qy          2273
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Qy          2333
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|
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[illegible]

TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 795

Qy 829 ACAGAGGGTGACCACCC-----  
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Db 796  
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Qy 880  
TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG----- 921  
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Db 856  
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Qy 922  
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Db 916  
GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTAAGCAGAAGCAT 975

Qy 982  
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Qy 1219  
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Qy 1906

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Db 1927

NNNNNNNGCCAACCTGTCTTCAGGAAGGTTTCATGCTAGAGAACATCCGATTCTCTCTACT 1986

Qy 1906 -----

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Db 1987

GTAATCACCATTGCAGNNGAATATGATGACAAGCAGCCACTGACCAGCAAAGAGGAAGAG 2046

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Qy 1987

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Qy 2107

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Db 2227

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Qy 2167

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Db 2287

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Qy 2227



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Qy 2287  
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Db 2407  
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Qy 2347  
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Db 2767  
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Qy 2707 TGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCATTGCTACATCAAGGGGT 2761  
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Db 2827 TGGCTCTTGACATTTTCTTCTCCTCCNTGGAGGCTACTGCCACATAAAAGGCT 2881

RESULT 11  
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 LOCUS CNSLT1IBJ 1589 bp mRNA linear HTC 18-  
 JUN-2003  
 DEFINITION human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of  
 Neuroblastoma of Homo sapiens (human).  
 ACCESSION BX248763  
 VERSION BX248763.1 GI:28375580  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1589)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ InVitroGen Corporation  
 1600  
 Faraday Avenue  
 REFERENCE 2 (bases 1 to 1589)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-FEB-2003) Genoscope - Centre National de  
 Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail :  
 seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer.  
 Five prime  
 end enriched, double-strand cDNA was digested with Not I and  
 cloned  
 into the Not I and Eco RV sites of the pCMVSPORT 6 vector.  
 Library  
 was normalized. Library was constructed by Life  
 Technologies, a  
 division of Invitrogen.  
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 /clone="CS0DB006YD18"  
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 /db\_xref="GI:28375581"  
 /translation="MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQN  
 NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASI

EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF  
IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLY  
MILAVFSPGVVQVWEGLLTLFFFVPCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIE  
TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDL"  
ORIGIN

Query Match 35.1%; Score 971; DB 3; Length 1589;  
Best Local Similarity 100.0%; Pred. No. 7.2e-258;  
Matches 971; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1  
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Qy 61  
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Qy 121  
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Db 739  
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Qy 421  
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Qy 541  
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Qy 601  
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Qy 661  
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Qy 721  
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 Db 1519  
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Qy 961 AAGGATCTGAA 971  
 |||||  
 Db 1579 AAGGATCTGAA 1589

RESULT 12

AK048160  
 LOCUS AK048160 3573 bp mRNA linear HTC 03-  
 APR-2004

DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length  
 enriched  
 library, clone:C130038C08 product:solute carrier family 8  
 (sodium/calcium exchanger), member 1, full insert sequence.

ACCESSION AK048160

VERSION AK048160.1 GI:26339181

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
 Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y.,  
 Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and  
 Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs  
 to  
 prepare full-length cDNA libraries for rapid discovery of

new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N.,  
 Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H.,  
 Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,  
 Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,  
 Kashiwagi,K.,  
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watahiki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S.,  
 Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
 Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team  
 and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration  
 Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional  
 annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3573)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H.,  
 Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T.,  
 Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I.,  
 Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M.,  
 Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K.,  
 Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-  
 Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute  
 of Physical and Chemical Research (RIKEN), Laboratory for  
 Genome Exploration Research Group, RIKEN Genomic Sciences Center  
 (GSC),  
 Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in  
 Riken Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN.  
 contributed to Division of Experimental Animal Research in Riken  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.jp/



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Qy          391  
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Qy          811 CGAGGAATTATCATAGAGACAGAGGGTGACCACCC-----  
TAAGGGCATTGAGATG 861  
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Db 1853  
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Db 1913  
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Db 1973  
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Qy 2314  
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 APR-2004  
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 cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.  
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 SOURCE Homo sapiens (human)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 938)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 8, 2003 this sequence version replaced gi:30438490.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer.  
 Five prime end enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector.  
 Library was normalized. Library was constructed by Life  
 Technologies, a division of Invitrogen. This sequence belongs to sequence  
 cluster 7256.r  
 For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?s=CS0DB006DB09\\_DB1287\\_2&c=7256.r](http://www.genoscope.cns.fr/cdna?s=CS0DB006DB09_DB1287_2&c=7256.r).  
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 normalized."  
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Matches 918; Conservative 0; Mismatches 20; Indels 1;  
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Qy 1107  
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RESULT 14

AY408695

LOCUS AY408695 2515 bp DNA linear GSS 12-

DEC-2003

DEFINITION Mus musculus HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY408695

VERSION AY408695.1 GI:39764666

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
Murinae; Mus.

REFERENCE 1 (bases 1 to 2515)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse  
orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2515)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,  
Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and  
ordering  
them based on alignment.

FEATURES Location/Qualifiers

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi;  
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 REFERENCE 1 (bases 1 to 887)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection  
 (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11613 row: m column: 05  
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 Site\_2: EcoRV (destroyed); RNA source anonymous  
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 and directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size  
 range 0.7-3.5 kb. Library is normalized and enriched for  
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Qy 1576

GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635

|||||

|  
Db 661

GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTA-T 719

Qy 1636

GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCC 1695

|||||

|||||

Db 720

GGTGTAATGGAGGTCAAGGTTCTGCGGACATCATGTGCCCCGGGGTACAGTCATCGTCCCC 779

Qy 1696 TTT-

AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGG 1754

||| ||||| ||||| ||||| ||| | | | |||||

|||||

Db 780

TTTCAGGACAGGAGAAGGGACAGCCAAGGCTGCACGCTAAGGACTTGAAGACCCATATGC 839

Qy 1755 GGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGT 1799

||||| || || ||||| ||||| ||||| |||

Db 840 GGAGTTGGAATTC-CGACTGGTGAACCTGTGAACACCATCACGGT 883

Search completed: January 22, 2005, 17:29:15

Job time : 8618.76 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 05:47:49 ; Search time 1295.46 Seconds  
(without alignments)  
11208.289 Million cell updates/sec

Title: US-10-054-680-1  
Perfect score: 2766  
Sequence: 1 atggcgtgggtaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2766	100.0	2766	6	ABQ78861	Abq78861 Human ion
2	2766	100.0	3812	6	ABQ78863	Abq78863 Human ion
3	2764.4	99.9	2766	6	ABQ78864	Abq78864 Human ion
4	2764.4	99.9	2828	12	ADH42302	Adh42302 Novel hum
5	2764.4	99.9	2966	6	ABZ33735	Abz33735 Human TRI

	6	2763	99.9	2778	12	ADH42314	Adh42314 Novel hum
	7	2763	99.9	2778	12	ADH42306	Adh42306 Novel hum
	8	2761.2	99.8	2782	6	ABN83428	Abn83428 Human tra
	9	2753	99.5	2769	6	ABQ78865	Abq78865 Human ion
	10	2751.4	99.5	2769	6	ABQ78866	Abq78866 Human ion
	11	2733.4	98.8	2781	6	ABA04756	Aba04756 Human nat
	12	2673.2	96.6	2685	8	ABX56263	Abx56263 Human NOV
	13	2673.2	96.6	2685	12	ADH42308	Adh42308 Novel hum
	14	2673.2	96.6	2685	12	ADH42312	Adh42312 Novel hum
	15	2657.6	96.1	2840	8	ABX56262	Abx56262 Human NOV
	16	2657.6	96.1	2840	12	ADH42304	Adh42304 Novel hum
	17	2367.2	85.6	2813	8	ABX56261	Abx56261 Human NOV
	18	2367.2	85.6	2813	12	ADH42310	Adh42310 Novel hum
	19	2367.2	85.6	2813	12	ADH42316	Adh42316 Novel hum
	20	1786.4	64.6	2534	10	ACC00414	Acc00414 Human 690
	21	1784.8	64.5	126512	6	ABN83429	Abn83429 Human tra
	22	1784.6	64.5	1863	6	ABQ78862	Abq78862 Human ion
	23	1326.4	48.0	2814	4	AAH57377	Aah57377 Human hea
	24	1294.4	46.8	3037	10	ADB59225	Adb59225 Toxicity-
	25	1277	46.2	4282	9	AAL55587	Aal55587 Human 465
	26	1277	46.2	4291	3	AAC75706	Aac75706 Human ORF
	27	1227.8	44.4	4087	6	AAD24450	Aad24450 Bovine NC
	28	1208.8	43.7	3250	12	ADP21419	Adp21419 Gene SLC8
	29	1208.8	43.7	5438	5	ABV24305	Abv24305 Human pro
	30	897.4	32.4	1187	5	AAS90968	Aas90968 DNA encod
	31	897.4	32.4	1187	8	ACD05939	Acd05939 Novel hum
c	32	878.4	31.8	2859	12	ADQ24550	Adq24550 Human sof
	33	821.4	29.7	823	12	ACH87070	Ach87070 Human gen
	34	787.2	28.5	1836	4	AAI19464	Aai19464 Probe #93
	35	787.2	28.5	1836	4	ABA64480	Aba64480 Human foe
	36	787.2	28.5	1836	4	AAI44657	Aai44657 Probe #13
	37	787.2	28.5	1836	4	ABA31619	Aba31619 Probe #10
	38	787.2	28.5	1836	4	AAK12937	Aak12937 Human bra
	39	787.2	28.5	1836	4	ABS38231	Abs38231 Human liv
	40	787.2	28.5	1836	6	ABS12734	Abs12734 Human gen
	41	593.2	21.4	4546	4	ABL09809	Abl09809 Drosophil
	42	503.4	18.2	505	12	ACH73341	Ach73341 Human gen
	43	494	17.9	551	12	ACH70908	Ach70908 Human gen
	44	366	13.2	366	12	ACH84609	Ach84609 Human gen
c	45	363	13.1	363	4	AAI85824	Aai85824 Human pol

#### ALIGNMENTS

##### RESULT 1

ABQ78861

ID ABQ78861 standard; cDNA; 2766 BP.

XX

AC ABQ78861;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;





Db	121	ACAGGGCAGAACAAATGAGTCTCTGTTACAGGGTTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCGGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCGGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860

Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGC TGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGC TGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTTGGC	2280
Db	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTTGGC	2280
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Db	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Qy	2341	GATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341	GATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCCACTAGAGGCCATTGTGCTACATCAAGGGG	2760

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760

Qy      2761 TTCTAA 2766
          ||||||
Db      2761 TTCTAA 2766

```

RESULT 2

ABQ78863

ID ABQ78863 standard; cDNA; 3812 BP.

XX

AC ABQ78863;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein cDNA #3.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;  
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;  
 KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are  
 PT structurally related to mammalian sodium-calcium exchanger proteins,  
 PT useful for drug screening, diagnosis and in gene therapy of biological  
 PT disorders.

XX

PS Disclosure; Page 41-42; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),  
 CC that shares structural similarity with mammalian sodium-calcium exchanger  
 CC proteins, and potassium dependent versions of the same. The NHIEP of the  
 CC invention has nootropic, cytostatic, antiarthritic, and virucide  
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can  
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease  
 CC or to therapeutically augment the efficacy of chemotherapeutic agents  
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The  
 CC sequence encodes a NHIEP of the invention, with regions of flanking  
 CC sequence

XX

SQ Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;



Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCTTGTTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCTTGTTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680

Db	2238		GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2297
Qy	1681		ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298		ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741		GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	2358		GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	2417
Qy	1801		AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2418		AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2477
Qy	1861		CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2478		CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2537
Qy	1921		GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2538		GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2597
Qy	1981		GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2598		GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2657
Qy	2041		ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGAGGGACCAGTTTCATGGAGGCCATC	2100
Db	2658		ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGAGGGACCAGTTTCATGGAGGCCATC	2717
Qy	2101		ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2718		ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2777
Qy	2161		TGCTTTGACTACGTCATGCACCTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2778		TGCTTTGACTACGTCATGCACCTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2837
Qy	2221		CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2838		CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2897
Qy	2281		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2340
Db	2898		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2957
Qy	2341		GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTTGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2958		GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTTGGCACCTCTGTCCCAGATACGTTTGCC	3017
Qy	2401		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	3018		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	3077
Qy	2461		AGCAACGCCGTCAATGTCTTCTTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520



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Db      3078 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137
Qy      2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGGCACACTGGCCTTCTCCGTCACC 2580
      .|||||
Db      3138 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGGCACACTGGCCTTCTCCGTCACC 3197
Qy      2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
      |||||
Db      3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257
Qy      2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
      |||||
Db      3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317
Qy      2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCATTGCTACATCAAGGGG 2760
      |||||
Db      3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCATTGCTACATCAAGGGG 3377
Qy      2761 TTCTAA 2766
      |||||
Db      3378 TTCTAA 3383

```

# RESULT 3

ABQ78864

ID ABQ78864 standard; cDNA; 2766 BP.

XX

AC ABQ78864;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;  
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;  
 KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /\*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.



Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTCTTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTCTTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320

Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGGTGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCGATTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCGATTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCCTGTGTG	2220

Db	2161		TGCTTTGACTACGTACATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Qy	2221		CCCCCACAGAGTACTGCCACGGCTGGGCCGTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2221		CCCCCACAGAGTACTGCCACGGCTGGGCCGTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Qy	2281		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Db	2281		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Qy	2341		GATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341		GATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461		AGCAACGCCGTCAATGTCTTCCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461		AGCAACGCCGTCAATGTCTTCCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521		TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2521		TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Qy	2581		CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2581		CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Qy	2641		CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641		CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701		AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2701		AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Qy	2761		TTCTAA 2766	
Db	2761		TTCTAA 2766	

#### RESULT 4

ADH42302

ID ADH42302 standard; DNA; 2828 BP.

XX

AC ADH42302;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55a.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;

KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;

KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;

KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;  
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102159-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 04-JUN-2003; 2003WO-US017573.  
XX  
PR 04-JUN-2002; 2002US-0385490P.  
PR 04-JUN-2002; 2002US-0385615P.  
PR 04-JUN-2002; 2002US-0385755P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 06-JUN-2002; 2002US-0386355P.  
PR 06-JUN-2002; 2002US-0386357P.  
PR 06-JUN-2002; 2002US-0386447P.  
PR 06-JUN-2002; 2002US-0386459P.  
PR 06-JUN-2002; 2002US-0386465P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 07-JUN-2002; 2002US-0386701P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0387078P.  
PR 07-JUN-2002; 2002US-0387081P.  
PR 07-JUN-2002; 2002US-0387083P.  
PR 10-JUN-2002; 2002US-0387429P.  
PR 10-JUN-2002; 2002US-0387540P.  
PR 10-JUN-2002; 2002US-0387866P.  
PR 11-JUN-2002; 2002US-0387606P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387659P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 12-JUN-2002; 2002US-0388432P.  
PR 12-JUN-2002; 2002US-0388479P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389604P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390144P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 25-JUN-2002; 2002US-0391726P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.

PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.  
PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.  
PR 01-NOV-2002; 2002US-0423095P.  
PR 05-NOV-2002; 2002US-0423748P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;  
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;  
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;  
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;  
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;  
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42303.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in  
PT pharmacogenomics.

XX

PS Claim 20; SEQ ID NO 855; 1503pp; English.

XX

CC The invention relates to 566 new isolated human polypeptides and their  
CC encoding genes, sequences that are at least 95% identical to these or  
CC sequences comprising one or more conservative substitutions in these. The  
CC polypeptide, polynucleotide and antibodies against the polypeptides are  
CC useful in diagnosing, treating or preventing NOVX-associated disorders,  
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,  
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.  
CC The nucleic acids are further used as hybridization probes, in chromosome  
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The  
CC polypeptides are also useful as vaccines. This sequence represents an  
CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2828 BP; 670 A; 692 C; 778 G; 688 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 12; Length 2828;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCTCTCCATTTTGGGCTGGTTACC	60
Db	63	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCTCTCCATTTTGGGCTGGTTACC	122
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	123	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	182
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	183	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	242
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	243	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	483	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900



Db	903	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1443	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTGAATGTGATACTATTTCAT	1620
Db	1623	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTGAATGTGATACTATTTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1683	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740

Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1863	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1922
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1923	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1982
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	1980
Db	1983	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	2042
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2043	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2102
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2103	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGGAGGGACCAGTTCATGGAGGCCATC	2162
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2163	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2222
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCGTGTGTG	2220
Db	2223	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCGTGTGTG	2282
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2283	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2342
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2340
Db	2343	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2402
Qy	2341	GATTCACTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2403	GATTCACTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2462
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2463	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2522
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2523	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2582
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2583	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2642

Qy 2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2643 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2702  
 Qy 2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2703 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2762  
 Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2763 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2822  
 Qy 2761 TTCTAA 2766  
 |||||  
 Db 2823 TTCTAA 2828

RESULT 5

ABZ33735

ID ABZ33735 standard; cDNA; 2966 BP.

XX

AC ABZ33735;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human TRICH encoding cDNA SEQ ID NO 41.

XX

KW Human; TRICH; transporter and ion channel; transport disorder;  
 KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;  
 KW neurological disorder; Alzheimer's disease; Huntington's disease;  
 KW immunological disorder; AIDS; asthma; cell proliferative disorder;  
 KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;  
 KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;  
 KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;  
 KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;  
 KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246415-A2.

XX

PD 13-JUN-2002.

XX

PF 05-DEC-2001; 2001WO-US046963.

XX

PR 08-DEC-2000; 2000US-0254303P.

PR 15-DEC-2000; 2000US-0256190P.

PR 21-DEC-2000; 2000US-0257504P.

PR 12-JAN-2001; 2001US-0261546P.

PR 19-JAN-2001; 2001US-0262832P.

PR 26-JAN-2001; 2001US-0264377P.

PR 02-FEB-2001; 2001US-0266019P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;

PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;  
 PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;  
 PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;  
 PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;  
 XX  
 DR WPI; 2002-519667/55.  
 DR P-PSDB; ABP74104.  
 XX  
 PT Novel human transporter and ion channel polypeptide, useful in diagnosis,  
 PT prevention or treatment of transport, neurological, muscle, immunological  
 PT and cell proliferative disorders.  
 XX  
 PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human transporter and ion channel polypeptide  
 CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-  
 CC ABP74127), a naturally occurring polypeptide comprising a sequence having  
 CC at least sequence 90 % identity to (I) or a biologically active or  
 CC immunogenic fragment of (I). (I) is useful for screening a compound for  
 CC effectiveness as an agonist or antagonist, for screening a compound that  
 CC specifically binds (I) or modulates the activity of (I) and for preparing  
 CC a polyclonal or monoclonal antibody by hybridoma technology.  
 CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for  
 CC screening a compound altering gene expression. (I) and (II) are useful in  
 CC a diagnostic tests for a condition or a disease associated with the  
 CC expression of TRICH in a biological sample, especially disorders selected  
 CC from a transport disorder such as cystic fibrosis, diabetes mellitus,  
 CC Parkinson's disease, cardiac disorders, neurological disorders such as  
 CC Alzheimer's disease, Huntington's disease, muscle disorders,  
 CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell  
 CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and  
 CC cancer. (II) is useful for creating knock-in humanised animals or  
 CC transgenic animals to model human diseases, in somatic or germline gene  
 CC therapy, to generate a transcript image of a tissue or cell type, for  
 CC detecting differences in the chromosomal location due to translocation,  
 CC inversion among normal, carrier or affected individuals and for mapping  
 CC genomic sequences. Note: The sequence data for this patent is not  
 CC represented in the printed specification but is based on sequence  
 CC information supplied to Derwent by the European Patent Office  
 XX  
 SQ Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 6; Length 2966;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	201	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	260
QY	61	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	261	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	320
QY	121	ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	321	ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	380

Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	381	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	440
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	441	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	500
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	501	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	560
Qy	361	ACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
Db	561	ACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	620
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	621	CTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	680
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	681	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	740
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	741	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	800
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	801	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	860
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220

Qy	1021	TACTATGCTCTTTTCCCAACCAACAGAAAGACCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTTCCCAACCAACAGAAAGACCGTGCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1401	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1460
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1521	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1580
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1581	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1640
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1641	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1700
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTTGGCCACA	1560
Db	1701	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTTGGCCACA	1760
Qy	1561	GTTACCATCTTGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1761	GTTACCATCTTGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1820
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1821	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1880
Qy	1681	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1881	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1940
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1941	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	2000
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2001	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2060
Qy	1861	CCGAAATGGATGGAAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920

Db	2061	 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2120
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2121	 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2180
Qy	1981	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2181	 GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2240
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2241	 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2300
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2301	 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2360
Qy	2161	TGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2361	 TGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2420
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCGTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2421	 CCCCCACAGAGTACTGCCACGGCTGGGCCGTGCTTCGCCGTCTCCATCCTCATCATTGGC	2480
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2340
Db	2481	 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2540
Qy	2341	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2541	 GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2600
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2601	 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2660
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCTCCGTGGCCGCCATCTAC	2520
Db	2661	 AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCTCCGTGGCCGCCATCTAC	2720
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2721	 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2780
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2781	 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2840
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2841	 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2900
Qy	2701	AGCCTGTGGCTCCTCTACATACTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760

Db 2901 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2960  
QY 2761 TTCTAA 2766  
|||  
Db 2961 TTCTAA 2966

RESULT 6

ADH42314

ID ADH42314 standard; DNA; 2778 BP.

XX

AC ADH42314;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55g.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;

KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;

KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;

KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;

KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;

KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;

KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

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OS Homo sapiens.

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PN WO2003102159-A2.

XX

PD 11-DEC-2003.

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PF 04-JUN-2003; 2003WO-US017573.

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PR 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386355P.

PR 06-JUN-2002; 2002US-0386357P.

PR 06-JUN-2002; 2002US-0386447P.

PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0386701P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0387078P.

PR 07-JUN-2002; 2002US-0387081P.

PR 07-JUN-2002; 2002US-0387083P.

PR 10-JUN-2002; 2002US-0387429P.

PR 10-JUN-2002; 2002US-0387540P.

PR 10-JUN-2002; 2002US-0387866P.

PR 11-JUN-2002; 2002US-0387606P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387659P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.



PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 12-JUN-2002; 2002US-0388432P.  
PR 12-JUN-2002; 2002US-0388479P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389604P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390144P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 25-JUN-2002; 2002US-0391726P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.  
PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.  
PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.  
PR 01-NOV-2002; 2002US-0423095P.  
PR 05-NOV-2002; 2002US-0423748P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;  
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;  
PI Khramtsov NV, Laroche WJ, Li L, Liang H, Low K, Macdougall JR;  
PI MacLachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;  
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;  
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;  
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42315.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in  
PT pharmacogenomics.

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PS Claim 20; SEQ ID NO 867; 1503pp; English.

XX

CC The invention relates to 566 new isolated human polypeptides and their  
CC encoding genes, sequences that are at least 95% identical to these or  
CC sequences comprising one or more conservative substitutions in these. The  
CC polypeptide, polynucleotide and antibodies against the polypeptides are  
CC useful in diagnosing, treating or preventing NOVX-associated disorders,  
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,  
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.  
CC The nucleic acids are further used as hybridization probes, in chromosome  
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The  
CC polypeptides are also useful as vaccines. This sequence represents an  
CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other:

Query Match 99.9%; Score 2763; DB 12; Length 2778;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	10	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	69
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	429
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600

Db	550		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661		CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670		CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841		CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850		CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901		CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910		CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	969
Qy	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201		GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210		GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381		CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440

Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCAC'TTTTGAATGTGATACTATTTCAT	1620
Db	1570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCAC'TTTTGAATGTGATACTATTTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGT'TATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1630	GTCAGTGAGAGTATTGGTGT'TATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1689
Qy	1681	ACAGTCATCGTCCCC'TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690	ACAGTCATCGTCCCC'TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1809
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAAT'TTCTTCATTGCCCTTGGTGAA	1860
Db	1810	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAAT'TTCTTCATTGCCCTTGGTGAA	1869
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1870	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1929
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	1980
Db	1930	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAC TA	1989
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1990	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2049
Qy	2041	ACAAACCTGGCC'TTGGTTGTGGGGACCCATTCTTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2050	ACAAACCTGGCC'TTGGTTGTGGGGACCCATTCTTGGAGGGACCAGTTCATGGAGGCCATC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2110	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCC'TGTGTG	2220
Db	2170	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCC'TGTGTG	2229
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTTGGC	2280
Db	2230	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTTGGC	2289

Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2340
Db	2290	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAA	2349
Qy	2341	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2350	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2410	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2469
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCTCCGTGGCCGCCATCTAC	2520
Db	2470	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCTCCGTGGCCGCCATCTAC	2529
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2530	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2589
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2590	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2649
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2650	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2709
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2710	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2769
Qy	2761	TTC	2763
Db	2770	TTC	2772

# RESULT 7

ADH42306

ID ADH42306 standard; DNA; 2778 BP.

XX

AC ADH42306;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55c.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;  
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;  
 KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;  
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;  
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX  
PN WO2003102159-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 04-JUN-2003; 2003WO-US017573.  
XX  
PR 04-JUN-2002; 2002US-0385490P.  
PR 04-JUN-2002; 2002US-0385615P.  
PR 04-JUN-2002; 2002US-0385755P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 06-JUN-2002; 2002US-0386355P.  
PR 06-JUN-2002; 2002US-0386357P.  
PR 06-JUN-2002; 2002US-0386447P.  
PR 06-JUN-2002; 2002US-0386459P.  
PR 06-JUN-2002; 2002US-0386465P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 07-JUN-2002; 2002US-0386701P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0387078P.  
PR 07-JUN-2002; 2002US-0387081P.  
PR 07-JUN-2002; 2002US-0387083P.  
PR 10-JUN-2002; 2002US-0387429P.  
PR 10-JUN-2002; 2002US-0387540P.  
PR 10-JUN-2002; 2002US-0387866P.  
PR 11-JUN-2002; 2002US-0387606P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387659P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 12-JUN-2002; 2002US-0388432P.  
PR 12-JUN-2002; 2002US-0388479P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389604P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390144P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 25-JUN-2002; 2002US-0391726P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.  
PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.

PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.  
PR 01-NOV-2002; 2002US-0423095P.  
PR 05-NOV-2002; 2002US-0423748P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;  
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;  
PI Khramtsov NV, Larochele WJ, Li L, Liang H, Low K, Macdougall JR;  
PI MacLachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;  
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;  
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;  
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42307.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in  
PT pharmacogenomics.

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PS Claim 20; SEQ ID NO 859; 1503pp; English.

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CC The invention relates to 566 new isolated human polypeptides and their  
CC encoding genes, sequences that are at least 95% identical to these or  
CC sequences comprising one or more conservative substitutions in these. The  
CC polypeptide, polynucleotide and antibodies against the polypeptides are  
CC useful in diagnosing, treating or preventing NOVX-associated disorders,  
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,  
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.  
CC The nucleic acids are further used as hybridization probes, in chromosome  
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The  
CC polypeptides are also useful as vaccines. This sequence represents an  
CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other;

Query Match 99.9%; Score 2763; DB 12; Length 2778;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60  
|||||

Db 10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

QY 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120  
|||||

Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCCTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	370	ACCAGCACAACCCTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	429
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	969



Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970		
		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030		
		TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090		
		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150		
		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210		
		GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270		
		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330		
		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390		
		CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450		
		TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTTGTGGCCACA	1560
Db	1510		
		GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTTGTGGCCACA	1569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1570		
		GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1630		
		GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690		
		ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1750		
		GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1809

Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1810	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1869
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1870	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1929
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1930	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1989
Qy	1981	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1990	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2049
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2050	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGAGGGACCAGTTCATGGAGGCCATC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2110	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2170	TGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2229
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2230	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Db	2290	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2349
Qy	2341	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTTGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2350	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTTGGCACCTCTGTCCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2410	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2469
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2470	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2529
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2530	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2589
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2590	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2649
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2650 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2709
Qy      2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2710 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769
Qy      2761 TTC 2763
      |||
Db      2770 TTC 2772

```

RESULT 8

ABN83428

ID ABN83428 standard; cDNA; 2782 BP.

XX

AC ABN83428;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein coding sequence.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;  
 KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 10. .2775

FT /\*tag= a

FT /product= "Human transporter"

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE ) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR P-PSDB; ABB83246.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily  
 PT for identifying modulators useful for treating a disease or condition  
 PT mediated by human transporter protein.

XX

PS Claim 4; Fig 1; 200pp; English.

XX

CC The present sequence is the coding sequence of a human transporter  
 CC protein, which is related to the sodium/calcium exchanger subfamily.

CC Experimental data indicates expression of the transporter gene in humans  
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal  
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR  
XX  
SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 99.8%; Score 2761.2; DB 6; Length 2782;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	10	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	69
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	189
Qy	181	CCAATCTGGTACCCGAGAAACCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGAGAAACCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	370	ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	429
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	729

Qy	721	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1510	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCCTTGTGTGGCCACA	1569

Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1570		
	1570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGTATTGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1630		
	1630	GTCAGTGAGAGTATTGGTGTATTGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690		
	1690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1750		
	1750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1809
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1810		
	1810	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1869
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1870		
	1870	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1929
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1930		
	1930	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATG	1989
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1990		
	1990	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2049
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTTCCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2050		
	2050	ACAAACCTGGCCTTGGTTGTGGGGACCCATTTCCTGGAGGGACCAGTTCATGGAGGCCATC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2110		
	2110	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2170		
	2170	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2229
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2230		
	2230	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2290		
	2290	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2349
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2350		
	2350	GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460

Db	2410	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2469
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2470	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2529
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2530	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2589
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2590	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2649
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2650	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2709
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2710	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2769
Qy	2761	TTCTAA	2766
Db	2770	TTCTAA	2775

RESULT 9

ABQ78865

ID ABQ78865 standard; cDNA; 2769 BP.

XX

AC ABQ78865;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;  
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;  
 KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	mutation	replace(2113..2115,-)
FT		/*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX





Db	361	ACCAGCACAAACCACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260

Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCC	1320
Db	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCC	1320
Qy	1321	AATGCAGGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGGAGGGAGCCAGTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTCGGAGGGAGCCAGTTCATGGAGGCCATC	2100



DE Human ion exchanger protein #1 cDNA A/G+GCA mutant.  
 XX  
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;  
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;  
 KW gene; ss; mutant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT mutation replace(1889,A)  
 FT /\*tag= a  
 FT mutation replace(2113. .2115,-)  
 FT /\*tag= b  
 XX  
 PN WO200259316-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001817.  
 XX  
 PR 23-JAN-2001; 2001US-0263384P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Friddle CJ, Hilbun E;  
 XX  
 DR WPI; 2002-599791/64.  
 XX  
 PT Novel polynucleotides encoding human ion exchanger proteins that are  
 PT structurally related to mammalian sodium-calcium exchanger proteins,  
 PT useful for drug screening, diagnosis and in gene therapy of biological  
 PT disorders.  
 XX  
 PS Disclosure; Page; 42pp; English.  
 XX  
 CC The invention relates to a novel human ion exchanger protein (NHIEP),  
 CC that shares structural similarity with mammalian sodium-calcium exchanger  
 CC proteins, and potassium dependent versions of the same. The NHIEP of the  
 CC invention has nootropic, cytostatic, antiarthritic, and virucide  
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can  
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease  
 CC or to therapeutically augment the efficacy of chemotherapeutic agents  
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The  
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The  
 CC present sequence is not shown in the specification but is derived from  
 CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)  
 XX  
 SQ Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

Query Match 99.5%; Score 2751.4; DB 6; Length 2769;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2765; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy	61	TTTGTGCTCTTCCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAACCTAGTAAAAACCATAAGGGTT	1800

Db	1741	 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	 CCGAAATGGATGGAACGTGGAATATCAGGTGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1981	 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2041	 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGT---GCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2157
Db	2101	 ACCGTCAGTGCAGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2160
Qy	2158	TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCGTGT	2217
Db	2161	 TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCGTGT	2220
Qy	2218	GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2277
Db	2221	 GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2280
Qy	2278	GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2337
Db	2281	 GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2340
Qy	2338	AAAGATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT	2397
Db	2341	 AAAGATTCAAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT	2400
Qy	2398	GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCCTCCATTGGCAACGTGACG	2457
Db	2401	 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCCTCCATTGGCAACGTGACG	2460
Qy	2458	GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC	2517
Db	2461	 GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC	2520
Qy	2518	TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTC	2577
Db	2521	 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTC	2580
Qy	2578	ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG	2637

Db 2581 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2640  
 Qy 2638 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2697  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2641 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2700  
 Qy 2698 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2757  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2701 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2760  
 Qy 2758 GGGTTCTAA 2766  
 ||||||||  
 Db 2761 GGGTTCTAA 2769

RESULT 11

ABA04756

ID ABA04756 standard; cDNA; 2781 BP.

XX

AC ABA04756;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;  
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;  
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;  
 KW coronary heart disease; renal failure; ischaemic disorder;  
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2781

FT /\*tag= a

FT /partial

FT /product= "Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3"

FT /note= "No stop codon given"

XX

PN WO200183744-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-EP004886.

XX

PR 02-MAY-2000; 2000EP-00109080.

XX

PA (MERE ) MERCK PATENT GMBH.

XX

PI Wilm C;

XX

DR WPI; 2002-041493/05.

DR P-PSDB; AAM47745.

XX

PT New polypeptide, useful as vaccines for inducing immune response against





Db	541	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	661	 CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	 CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	 TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	 AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440

Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCAC'TTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCAC'TTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGT'TATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGT'TATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCC'TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCC'TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAAT'TCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAAT'TCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATC-----AGATGTGACAGACAGG	1902
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGGTGTGAGATTCTTTAAAGATGTGACAGACAGG	1920
Qy	1903	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1962
Db	1921	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1980
Qy	1963	GGTGAACACCCCAAAC'TAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2022
Db	1981	GGTGAACACCCCAAAC'TAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2040
Qy	2023	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGAGGGGAC	2082
Db	2041	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGAGGGGAC	2100
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2142
Db	2101	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2160
Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCAC'TTCTGACTGTCTTCTGGAAG	2202
Db	2161	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCAC'TTCTGACTGTCTTCTGGAAG	2220
Qy	2203	GTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2262
Db	2221	GTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2280

Qy	2263	TCCATCCTCATCATTTGGCATGCTCACCGCCATCATTTGGGGACCTGGCCTCGCACTTCGGC	2322
Db	2281	TCCATCCTCATCATTTGGCATGCTCACCGCCATCATTTGGGGACCTGGCCTCGCACTTCGGC	2340
Qy	2323	TGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCT	2382
Db	2341	TGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCT	2400
Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCCTCC	2442
Db	2401	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCCTCC	2460
Qy	2443	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCCTTCCTGGGCATCGGCCCTGGCCCTGG	2502
Db	2461	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCCTTCCTGGGCATCGGCCCTGGCCCTGG	2520
Qy	2503	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA	2562
Db	2521	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA	2580
Qy	2563	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2622
Db	2581	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2640
Qy	2623	TACCGAAGGCGGCCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2682
Db	2641	TACCGAAGGCGGCCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2700
Qy	2683	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2742
Db	2701	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2760
Qy	2743	TATTGCTACATCAAGGGGTTTC	2763
Db	2761	TATTGCTACATCAAGGGGTTTC	2781

# RESULT 12

ABX56263

ID ABX56263 standard; DNA; 2685 BP.

XX

AC ABX56263;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 DNA SEQ ID 5.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;  
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;  
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;  
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;  
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;  
 KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX  
PN WO200281625-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002WO-US010366.  
XX  
PR 03-APR-2001; 2001US-0281086P.  
PR 05-APR-2001; 2001US-0281906P.  
PR 06-APR-2001; 2001US-0282020P.  
PR 10-APR-2001; 2001US-0282930P.  
PR 12-APR-2001; 2001US-0283444P.  
PR 12-APR-2001; 2001US-0283512P.  
PR 13-APR-2001; 2001US-0283657P.  
PR 13-APR-2001; 2001US-0283678P.  
PR 13-APR-2001; 2001US-0283710P.  
PR 17-APR-2001; 2001US-0284234P.  
PR 19-APR-2001; 2001US-0285325P.  
PR 20-APR-2001; 2001US-0285381P.  
PR 24-APR-2001; 2001US-0286068P.  
PR 25-APR-2001; 2001US-0286292P.  
PR 07-JUN-2001; 2001US-0296692P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 08-AUG-2001; 2001US-0311003P.  
PR 13-AUG-2001; 2001US-0311973P.  
PR 16-AUG-2001; 2001US-0312901P.  
PR 14-SEP-2001; 2001US-0322283P.  
PR 05-OCT-2001; 2001US-0327448P.  
PR 31-DEC-2001; 2001US-0345734P.  
PR 03-JAN-2002; 2002US-0345755P.  
PR 04-FEB-2002; 2002US-0354391P.  
PR 02-APR-2002; 2002US-00114153.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;  
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;  
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;  
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;  
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;  
PI Mazur A;  
XX  
DR WPI; 2003-046862/04.  
DR P-PSDB; ABU12043.  
XX  
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,  
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious  
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and  
PT cancer.  
XX  
PS Claim 3; Page 85-86; 425pp; English.  
XX  
CC This invention describes novel polypeptides, termed NOVX which have  
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,  
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,  
CC cardiant and immunomodulatory activity. The polypeptide and any  
CC antibodies generated from it are useful in the manufacture of a



Qy	626	GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	685
Db	542	GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	601
Qy	686	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	745
Db	602	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	661
Qy	746	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	805
Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1285
Db	1142	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGGCTGACTATGAGTTCA	1345
Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381

Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTATGG	1645
Db	1502	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTATGG	1561
Qy	1646	AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCCTTAGGACAG	1705
Db	1562	AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCCTTAGGACAG	1621
Qy	1706	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
Qy	1766	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAAATAGTAGATGAGGAGGAATACG	1825
Db	1682	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAAATAGTAGATGAGGAGGAATACG	1741
Qy	1826	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1885
Db	1742	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1801
Qy	1886	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1945
Db	1802	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1861
Qy	1946	TGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTGAAGTCATCATTGAAGAGTCCTATG	2005
Db	1862	TGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTGAAGTCATCATTGAAGAGTCCTATG	1921
Qy	2006	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	2065
Db	1922	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	1981
Qy	2066	CCCATTCCTGGAGGGACCAAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2125
Db	1982	CCCATTCCTGGAGGGACCAAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2041
Qy	2126	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2185
Db	2042	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2101
Qy	2186	TGACTGTCTTCTGGAAGGTGCTGTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2245
Db	2102	TGACTGTCTTCTGGAAGGTGCTGTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2161
Qy	2246	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2305
Db	2162	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2221
Qy	2306	TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTCG	2365



Db	2222		TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTTCG	2281
Qy	2366		TGGCATTTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2425
Db	2282		TGGCATTTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2341
Qy	2426		TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTCTGG	2485
Db	2342		TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTCTGG	2401
Qy	2486		GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2545
Db	2402		GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2461
Qy	2546		ACGTGTCTGGCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCT	2605
Db	2462		ACGTGTCTGGCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCT	2521
Qy	2606		GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2665
Db	2522		GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2581
Qy	2666		GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2725
Db	2582		GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2641
Qy	2726		TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2763
Db	2642		TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2679

RESULT 13

ADH42308

ID ADH42308 standard; DNA; 2685 BP.

XX

AC ADH42308;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55d.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;  
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;  
 KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;  
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;  
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX

PN WO2003102159-A2.

XX

PD 11-DEC-2003.

XX

PF 04-JUN-2003; 2003WO-US017573.

XX

PR 04-JUN-2002; 2002US-0385490P.  
PR 04-JUN-2002; 2002US-0385615P.  
PR 04-JUN-2002; 2002US-0385755P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 06-JUN-2002; 2002US-0386355P.  
PR 06-JUN-2002; 2002US-0386357P.  
PR 06-JUN-2002; 2002US-0386447P.  
PR 06-JUN-2002; 2002US-0386459P.  
PR 06-JUN-2002; 2002US-0386465P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 07-JUN-2002; 2002US-0386701P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0387078P.  
PR 07-JUN-2002; 2002US-0387081P.  
PR 07-JUN-2002; 2002US-0387083P.  
PR 10-JUN-2002; 2002US-0387429P.  
PR 10-JUN-2002; 2002US-0387540P.  
PR 10-JUN-2002; 2002US-0387866P.  
PR 11-JUN-2002; 2002US-0387606P.  
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PR 11-JUN-2002; 2002US-0387668P.  
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PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 12-JUN-2002; 2002US-0388432P.  
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PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389146P.  
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PR 18-JUN-2002; 2002US-0389604P.  
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PR 19-JUN-2002; 2002US-0390006P.  
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PR 19-JUN-2002; 2002US-0390209P.  
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PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.  
PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.  
PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.

Db 122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy	266	TTGGGGTGTCCATCATTTGCTGACCGCTTTCATGGGCATCTATTGAAGTCATCACCTCTCAAG	325
Db	182	TTGGGGTGTCCATCATTTGCTGACCGCTTTCATGGGCATCTATTGAAGTCATCACCTCTCAAG	241
Qy	326	AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACTATTTCGGGTCT	385
Db	242	AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACTATTTCGGGTCT	301
Qy	386	GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATAC	445
Db	302	GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATAC	361
Qy	446	TCCTCTCTTTAATTGAGGTGTGTGGTTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA	505
Db	362	TCCTCTCTTTAATTGAGGTGTGTGGTTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA	421
Qy	506	CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGA	565
Db	422	CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGA	481
Qy	566	TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTTCATCACCGCTGCTT	625
Db	482	TCCCAGACGGAGAGACTCGCAAGATCAACATCTACGAGTCTTCTTTCATCACCGCTGCTT	541
Qy	626	GGAGTATCTTTGCCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	685
Db	542	GGAGTATCTTTGCCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	601
Qy	686	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT	745
Db	602	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT	661
Qy	746	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	805
Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAAACATGCAGCAGAACCAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165

Db	1022	 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACCA	1285
Db	1142	 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	 CTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1645
Db	1502	 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1561
Qy	1646	AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCCTTTAGGACAG	1705
Db	1562	 AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCCTTTAGGACAG	1621
Qy	1706	TAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	 TAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
Qy	1766	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAAATAGTAGATGAGGAGGAATACG	1825
Db	1682	 TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAAATAGTAGATGAGGAGGAATACG	1741
Qy	1826	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1885
Db	1742	 AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1801
Qy	1886	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1945
Db	1802	 CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1861
Qy	1946	TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATG	2005



ID ADH42312 standard; DNA; 2685 BP.  
XX  
AC ADH42312;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Novel human nucleic acid NOV55f.  
XX  
KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;  
KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;  
KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;  
KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;  
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;  
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102159-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 04-JUN-2003; 2003WO-US017573.  
XX  
PR 04-JUN-2002; 2002US-0385490P.  
PR 04-JUN-2002; 2002US-0385615P.  
PR 04-JUN-2002; 2002US-0385755P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 06-JUN-2002; 2002US-0386355P.  
PR 06-JUN-2002; 2002US-0386357P.  
PR 06-JUN-2002; 2002US-0386447P.  
PR 06-JUN-2002; 2002US-0386459P.  
PR 06-JUN-2002; 2002US-0386465P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 07-JUN-2002; 2002US-0386701P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0387078P.  
PR 07-JUN-2002; 2002US-0387081P.  
PR 07-JUN-2002; 2002US-0387083P.  
PR 10-JUN-2002; 2002US-0387429P.  
PR 10-JUN-2002; 2002US-0387540P.  
PR 10-JUN-2002; 2002US-0387866P.  
PR 11-JUN-2002; 2002US-0387606P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387659P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 12-JUN-2002; 2002US-0388432P.  
PR 12-JUN-2002; 2002US-0388479P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389604P.  
PR 18-JUN-2002; 2002US-0389884P.  
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PR 19-JUN-2002; 2002US-0390144P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 25-JUN-2002; 2002US-0391726P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402268P.  
PR 12-AUG-2002; 2002US-0402822P.  
PR 13-AUG-2002; 2002US-0403458P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 15-AUG-2002; 2002US-0403732P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 12-SEP-2002; 2002US-0410085P.  
PR 13-SEP-2002; 2002US-0410505P.  
PR 23-SEP-2002; 2002US-0412955P.  
PR 30-SEP-2002; 2002US-0415195P.  
PR 23-OCT-2002; 2002US-0420627P.  
PR 23-OCT-2002; 2002US-0420718P.  
PR 24-OCT-2002; 2002US-0420852P.  
PR 31-OCT-2002; 2002US-0422750P.  
PR 01-NOV-2002; 2002US-0423095P.  
PR 05-NOV-2002; 2002US-0423748P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;  
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;  
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;  
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;  
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;  
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;  
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;  
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42313.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in  
PT pharmacogenomics.

XX

PS Claim 20; SEQ ID NO 865; 1503pp; English.

XX

CC The invention relates to 566 new isolated human polypeptides and their  
CC encoding genes, sequences that are at least 95% identical to these or  
CC sequences comprising one or more conservative substitutions in these. The  
CC polypeptide, polynucleotide and antibodies against the polypeptides are  
CC useful in diagnosing, treating or preventing NOVX-associated disorders,  
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,  
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.



CC The nucleic acids are further used as hybridization probes, in chromosome  
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The  
CC polypeptides are also useful as vaccines. This sequence represents an  
CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2685 BP; 645 A; 657 C; 741 G; 642 T; 0 U; 0 Other;

Query Match 96.6%; Score 2673.2; DB 12; Length 2685;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2675; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTT 145
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Db       2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTT 61

Qy     146 CAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
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Db      62 CAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy     206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
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Db     122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy     266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
      |||||
Db     182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy     326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAAACCCTATTCGGGTCT 385
      |||||
Db     242 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAAACCCTATTCGGGTCT 301

Qy     386 GGAATGAAACTGTCTCCAACCTGACCCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATAC 445
      |||||
Db     302 GGAATGAAACTGTCTCCAACCTGACCCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATAC 361

Qy     446 TCCTCTCTTTAATTGAGGTGTGTGGTTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA 505
      |||||
Db     362 TCCTCTCTTTAATTGAGGTGTGTGGTTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA 421

Qy     506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGA 565
      |||||
Db     422 CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGA 481

Qy     566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTTCATCACCGCTGCTT 625
      |||||
Db     482 TCCCAGACGGAGAGACTCGCAAGATCAACATCTACGAGTCTTCTTTCATCACCGCTGCTT 541

Qy     626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
      |||||
Db     542 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 601

Qy     686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
      |||||
Db     602 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 661

Qy     746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
      |||||
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Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAAGGGGGAGACATGTCAAAGACCA	1285
Db	1142	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAAGGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	TTGATGACGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	CTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTTATGG	1645
Db	1502	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTTATGG	1561

Qy	1646	AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCCTTTAGGACAG	1705
Db	1562	AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCCTTTAGGACAG	1621
Qy	1706	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
Qy	1766	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1825
Db	1682	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1741
Qy	1826	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1885
Db	1742	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1801
Qy	1886	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1945
Db	1802	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1861
Qy	1946	TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTTGAAGAGTCCTATG	2005
Db	1862	TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTTGAAGAGTCCTATG	1921
Qy	2006	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	2065
Db	1922	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	1981
Qy	2066	CCCATTCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2125
Db	1982	CCCATTCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2041
Qy	2126	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2185
Db	2042	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2101
Qy	2186	TGACTGTCTTCTGGAAGGTGCTGTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2245
Db	2102	TGACTGTCTTCTGGAAGGTGCTGTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2161
Qy	2246	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2305
Db	2162	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2221
Qy	2306	TGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCG	2365
Db	2222	TGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCG	2281
Qy	2366	TGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2425
Db	2282	TGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2341
Qy	2426	TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAACGCCGTCAATGTCTTCCTGG	2485
Db	2342	TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAACGCCGTCAATGTCTTCCTGG	2401

Qy	2486	GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2545
Db	2402	GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2461
Qy	2546	ACGTGTTCGGCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCT	2605
Db	2462	ACGTGTTCGGCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCT	2521
Qy	2606	GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2665
Db	2522	GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2581
Qy	2666	GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2725
Db	2582	GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2641
Qy	2726	TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2763
Db	2642	TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2679

RESULT 15

ABX56262

ID ABX56262 standard; DNA; 2840 BP.

XX

AC ABX56262;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1b CG56558-02 DNA SEQ ID 3.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;  
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;  
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;  
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;  
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;  
 KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

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PF 03-APR-2002; 2002WO-US010366.

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PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.  
PR 20-APR-2001; 2001US-0285381P.  
PR 24-APR-2001; 2001US-0286068P.  
PR 25-APR-2001; 2001US-0286292P.  
PR 07-JUN-2001; 2001US-0296692P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 08-AUG-2001; 2001US-0311003P.  
PR 13-AUG-2001; 2001US-0311973P.  
PR 16-AUG-2001; 2001US-0312901P.  
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PR 05-OCT-2001; 2001US-0327448P.  
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PR 03-JAN-2002; 2002US-0345755P.  
PR 04-FEB-2002; 2002US-0354391P.  
PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;  
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;  
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;  
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;  
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;  
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR P-PSDB; ABU12042.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,  
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious  
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and  
PT cancer.

XX

PS Claim 3; Page 84; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have  
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,  
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,  
CC cardiant and immunomodulatory activity. The polypeptide and any  
CC antibodies generated from it are useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease  
CC selected from a pathology associated with the NOVX polypeptide. Fragments  
CC and portions of the polynucleotides encoding NOVX polypeptides are useful  
CC to map the location of NOVX genes on a chromosome, to identify  
CC individuals from minute biological samples, as DNA markers for  
CC restriction fragment length polymorphism (RFLP), and are useful to  
CC prepare polymerase chain reaction primers. The products of the invention  
CC can be used in gene therapy and for treating cardiomyopathy, metabolic  
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,  
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's  
CC disease, immune disorders, haematopoietic disorders, and various  
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic  
CC syndrome X and wasting disorders associated with chronic diseases and  
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments  
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086

XX

SQ Sequence 2840 BP; 668 A; 700 C; 775 G; 697 T; 0 U; 0 Other;

Query Match 96.1%; Score 2657.6; DB 8; Length 2840;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	63	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	122
Qy	61	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	123	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	182
Qy	121	ACAGGGCAGAACAATGAGTCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	183	ACAGGGCAGAACAATGAGTCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	242
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	243	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAA'TTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAA'TTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTCCGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	483	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842

Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680

Db	1683	GTCTAGTCTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTCAAAACAATTACATC	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1863	AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC	1922
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTG-----ACAGACAGGAAGCTG	1908
Db	1923	CCCCGCATGGTGGATATGAGTTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG	1982
Qy	1909	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	1968
Db	1983	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	2042
Qy	1969	CACCCCAAACCTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2028
Db	2043	CACCCCAAACCTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2102
Qy	2029	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGAGGGGACCAGTTC	2088
Db	2103	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGAGGGGACCAGTTC	2162
Qy	2089	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2148
Db	2163	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2222
Qy	2149	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTG	2208
Db	2223	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTG	2282
Qy	2209	TTTGCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2268
Db	2283	TTTGCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2342
Qy	2269	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2328
Db	2343	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2402
Qy	2329	ATTGGTCTCAAAGATTCAAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCA	2388
Db	2403	ATTGGTCTCAAAGATTCAAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCA	2462
Qy	2389	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2448
Db	2463	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2522
Qy	2449	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2508



Db	2523	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2582
Qy	2509	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCAGACTGGCC	2568
Db	2583	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCAGACTGGCC	2642
Qy	2569	TTCTCCGTCAACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2628
Db	2643	TTCTCCGTCAACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2702
Qy	2629	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2688
Db	2703	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2762
Qy	2689	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2748
Db	2763	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2822
Qy	2749	TACATCAAGGGGTTCTAA	2766
Db	2823	TACATCAAGGGGTTCTAA	2840

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:18:20 ; Search time 226.467 Seconds  
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updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Match	Query Length	DB	ID	Description	
-----							
c	1	78.8	2.8	7218	1	US-08-232-463-14	
Appl	2	76.6	2.8	1935	4	US-09-701-068-3	
Appli	3	76.6	2.8	1950	4	US-09-701-068-1	
Appli	4	51.6	1.9	7218	1	US-08-232-463-14	
Appl	5	50.8	1.8	951	4	US-09-961-679-3	

Appli 6	50.8	1.8	1062	4	US-09-961-679-5	Sequence 5,
Appli 7	50.8	1.8	1812	4	US-09-961-679-1	Sequence 1,
Appli 8	50.8	1.8	2366	4	US-09-961-679-7	Sequence 7,
Appli c 9	50.2	1.8	390	3	US-09-197-649-7	Sequence 7,
Appli 10	46.2	1.7	3984	4	US-09-016-434-1199	Sequence
1199, Ap 11	46.2	1.7	4473	4	US-09-799-451-118	Sequence
118, App 12	46.2	1.7	4559	4	US-09-919-172-61	Sequence 61,
Appl 13	44.8	1.6	2803	4	US-09-701-068-4	Sequence 4,
Appli c 14	44.2	1.6	4403765	3	US-09-103-840A-2	Sequence 2,
Appli c 15	43.8	1.6	1992	4	US-09-252-991A-9693	Sequence
9693, Ap 16	43.8	1.6	2658	4	US-09-252-991A-9558	Sequence
9558, Ap 17	43.8	1.6	2799	4	US-09-252-991A-9604	Sequence
9604, Ap c 18	43.4	1.6	4411529	3	US-09-103-840A-1	Sequence 1,
Appli 19	42.8	1.5	1174	4	US-09-270-767-25428	Sequence
25428, A 20	42.8	1.5	1612	4	US-09-270-767-10086	Sequence
10086, A 21	42.2	1.5	660	4	US-09-252-991A-5866	Sequence
5866, Ap 22	42.2	1.5	1983	4	US-09-252-991A-5825	Sequence
5825, Ap c 23	42.2	1.5	1995	4	US-09-252-991A-5783	Sequence
5783, Ap 24	41.8	1.5	870	4	US-09-252-991A-3650	Sequence
3650, Ap 25	41.8	1.5	1098	4	US-09-252-991A-3605	Sequence
3605, Ap c 26	41.8	1.5	3402	4	US-09-252-991A-1374	Sequence
1374, Ap 27	41.8	1.5	3687	4	US-09-252-991A-1193	Sequence
1193, Ap 28	41.8	1.5	4266	4	US-09-252-991A-1234	Sequence
1234, Ap 29	41.4	1.5	4403765	3	US-09-103-840A-2	Sequence 2,
Appli 30	41.4	1.5	4411529	3	US-09-103-840A-1	Sequence 1,
Appli 31	40.6	1.5	2036	4	US-09-799-451-772	Sequence
772, App 32	40.2	1.5	1174	3	US-09-034-985-1	Sequence 1,
Appli 33	40	1.4	570	4	US-09-252-991A-10419	Sequence
10419, A c 34	40	1.4	789	4	US-09-252-991A-10654	Sequence
10654, A c 35	40	1.4	813	4	US-09-252-991A-10547	Sequence

10547, A									
36	40	1.4	831	4	US-09-252-991A-10512	Sequence			
10512, A									
37	39.6	1.4	1827	4	US-09-270-767-1308	Sequence			
1308, Ap									
38	39.6	1.4	1827	4	US-09-270-767-16590	Sequence			
16590, A									
39	39.6	1.4	3431	4	US-09-221-017B-993	Sequence			
993, App									
40	39.2	1.4	333	4	US-09-252-991A-3700	Sequence			
3700, Ap									
c 41	39	1.4	642	4	US-09-252-991A-4949	Sequence			
4949, Ap									
42	39	1.4	1617	4	US-09-489-039A-2262	Sequence			
2262, Ap									
43	39	1.4	1926	4	US-09-249-585A-4	Sequence 4,			
Appli									
44	39	1.4	1931	2	US-09-130-114-2	Sequence 2,			
Appli									
45	39	1.4	1932	4	US-09-252-991A-4998	Sequence			
4998, Ap									

#### ALIGNMENTS

#### RESULT 1

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768





Qy 2414  
CCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCA 2473  
| | | | | | | | | | | | | | | | | | | | | |

Db 1409  
CAGAGCGACAACCTAACCGCAGATTGAGCTATTGCAAACATCACCTGCAGTAACTCGGTGA 1468

Qy 2474 ATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1469 ACATCTATGTGGGGATTGGAGTTCGGTGGCTGATAAACACAGTCTAC 1515

RESULT 3

US-09-701-068-1

; Sequence 1, Application US/09701068  
; Patent No. 6677506  
; GENERAL INFORMATION:  
; APPLICANT: Galil, Gad et al.  
; TITLE OF INVENTION: DNA CODING FOR A Mg<sup>2+</sup>/H<sup>+</sup> OR Zn<sup>2+</sup>/H<sup>+</sup> EXCHANGER AND  
TRANSGENIC PLANTS  
; TITLE OF INVENTION: EXPRESSING SAME  
; FILE REFERENCE: 01/21317  
; CURRENT APPLICATION NUMBER: US/09/701,068  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1950  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-701-068-1

Query Match 2.8%; Score 76.6; DB 4; Length 1950;  
Best Local Similarity 51.3%; Pred. No. 1.2e-12;  
Matches 178; Conservative 0; Mismatches 169; Indels 0;  
Gaps 0;

Qy 2174  
TCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGT 2233  
| | | | | | | | | | | | | | | | | | | | | |

Db 1174  
TCTGGCATTACTCCTCGCCCCTTGGAACTGCTTTTTGCATTTGTGCCCCCTGCAACA 1233

Qy 2234  
ACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCA 2293  
| | | | | | | | | | | | | | | | | | | | | |

Db 1234  
TTGCTCACGGTTGGATCGCTTTCATCTGCTCTCTCCTCTTCATCAGTGGAGTAGCCTTTG 1293

Qy 2294  
TCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTGAGTCACAG 2353  
| | | | | | | | | | | | | | | | | | | | | |

Db 1294  
TTGTCACAAGATTTACTGACCTTATAAGCTGTGTCACTGGAATAAACCCATATGTGATAG 1353

Qy 2354  
CTGTTGTTTTCGTGGCATTGACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTG 2413  
| | | | | | | | | | | | | | | | | | | | | |

```

||||
Db      1354
CATTACAGCACTCGCAAGTGGAAC TTCATGGCCAGACTTAGTAGCAAGTAAAATCGCTG 1413

Qy      2414
CCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCA 2473
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|
Db      1414
CAGAGCGACAAC TAACCGCAGATT CAGCTATTGCAAACATCACCTGCAGTAACTCGGTGA 1473

Qy      2474 ATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1474 ACATCTATGTGGGGATTGGAGTTC CGTGGCTGATAAACACAGTCTAC 1520

```

RESULT 4

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single



```

;      TOPOLOGY:  linear
;      IMMEDIATE SOURCE:
;      CLONE:     pTZgpt-Fls
US-08-232-463-14

```

Query Match 1.9%; Score 51.6; DB 1; Length 7218;  
Best Local Similarity 5.9%; Pred. No. 0.00017;  
Matches 24; Conservative 215; Mismatches 169; Indels 0;  
Gaps 0;

[illegible][illegible][illegible][illegible]

```
Qy      635  
TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTTGGTCCAGGTTT   694  
          :: :: : :: : :::: : : :::: : :::::::::::::: : : :::  
:::  
Db     1318  
YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377
```

**Qy**               695  
GGGAAGGCCTCCTCACTCTCTTCTTTCCAGTGtGTGTCCTTCTGGcCTGGGTGGCAG 754  
                ::: : ::: : : : : : : : : : : : : : :  
**Db**              1378  
YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTAA 1437

Qy 755 ATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAG 802  
 ||| | ||| ||| ||| ||| ||| ||| ||| |||  
 Db 1438 CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485

RESULT 5  
US-09-961-679-3  
; Sequence 3, Application US/09961679  
; Patent No. 6787352  
; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan  
; APPLICANT: Gerhardt, Brenda  
; TITLE OF INVENTION: No. 6787352el Human Ion-Exchanger Proteins and  
Polynucleotides Encoding the  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0239-USA  
; CURRENT APPLICATION NUMBER: US/09/961,679  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/235,745  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 951  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-961-679-3

Query Match 1.8%; Score 50.8; DB 4; Length 951;  
Best Local Similarity 51.9%; Pred. No. 6.7e-05;  
Matches 140; Conservative 0; Mismatches 127; Indels 3;  
Gaps 1;

Qy 2247  
GGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCT 2306  
|| | ||| | | || | | | | | | | | |

||  
Db 444  
GGTCACCTTCATCACCGCCACGCTGTGGATCGCTGTGTTCTCCTACATCATGGTGTGGCT 503

Qy 2307  
GGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGT 2366  
|| | ||| | || | || | || | || | || |

|  
Db 504  
GGTGACTATTATCGGATACACACTTGGGATCCCGGATGTCATCATGGGCATTACTTTCCT 563

Qy 2367  
GGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGT 2426  
||| | || | || ||| | |||| | || | || |

|  
Db 564  
GGCAGCAGGGACAAGTGTTCAGACTGCATGGCCAGCCTAATTGTGGCGAGACAAGGCCT 623

Qy 2427  
ATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGG 2486  
|| || | | ||| | || |||| | | || |

||  
Db 624 --- ..  
TGGGGACATGGCAGTCTCCAACACCATAGGAAGCAACGTGTTTGACATCCTGGTAGG 680

Qy 2487 CATCGGCCTGGCCTGGTCCGTGGCCGCCAT 2516  
| || | | || | || |||  
Db 681 ACTTGGTGTACCGTGGGGCCTGCAGACCAT 710

RESULT 6  
US-09-961-679-5  
; Sequence 5, Application US/09961679  
; Patent No. 6787352

; GENERAL INFORMATION:  
; APPLICANT: Friddle, Carl Johan  
; APPLICANT: Gerhardt, Brenda  
; TITLE OF INVENTION: No. 6787352el Human Ion-Exchanger Proteins and Polynucleotides Encoding the  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0239-USA  
; CURRENT APPLICATION NUMBER: US/09/961,679  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/235,745  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1062  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-961-679-5

Query Match 1.8%; Score 50.8; DB 4; Length 1062;  
Best Local Similarity 51.9%; Pred. No. 7.3e-05;  
Matches 140; Conservative 0; Mismatches 127; Indels 3;  
Gaps 1;

Qy 2247  
GGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCT 2306  
|| | ||| | | || | | | | | | | | | |

||  
Db 555  
GGTCACCTTCATCACCGCCACGCTGTGGATCGCTGTGTTCTCCTACATCATGGTGTGGCT 614

Qy 2307  
GGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTTCGT 2366  
|| | ||| | || | || | || | || | || | || |

|  
Db 615  
GGTGACTATTATCGGATACACACTTGGGATCCCGGATGTCATCATGGGCATTACTTTCCT 674

Qy 2367  
GGCATTGGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGT 2426  
||| | || | || |||| | |||| | || | || |

|  
Db 675  
GGCAGCAGGGACAAGTGTTCAGACTGCATGGCCAGCCTAATTGTGGCGAGACAAGGCCT 734

Qy 2427  
ATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGG 2486  
|| || | | ||| | || |||| | || |

||  
Db 735 ---  
TGGGGACATGGCAGTCTCCAACACCATAGGAAGCAACGTGTTTGACATCCTGGTAGG 791

Qy 2487 CATCGGCCTGGCCTGGTCCGTGGCCGCCAT 2516  
| | | | | || | || |||  
Db 792 ACTTGGTGTACCGTGGGGCCTGCAGACCAT 821

RESULT 7  
US-09-961-679-1  
; Sequence 1, Application US/09961679

```
; Patent No. 6787352
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: No. 6787352el Human Ion-Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0239-USA
; CURRENT APPLICATION NUMBER: US/09/961,679
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,745
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-961-679-1
```

```
Query Match          1.8%; Score 50.8; DB 4; Length 1812;
Best Local Similarity 51.9%; Pred. No. 0.00011;
Matches 140; Conservative 0; Mismatches 127; Indels 3;
Gaps 1;
```

```
Qy      2247
GGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCT 2306
      || | ||| | | ||| || | || | || ||| | |
```

```
Db      1305
GGTCACCTTCATCACCGCCACGCTGTGGATCGCTGTGTTCTCCTACATCATGGTGTGGCT 1364
```

```
Qy      2307
GGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTCACTCACAGCTGTTGTTTTCGT 2366
      || | | ||| | ||| ||| || | || | || | |||
```

```
Db      1365
GGTGACTATTATCGGATACACACTTGGGATCCCGGATGTCATCATGGGCATTACTTTCCT 1424
```

```
Qy      2367
GGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGT 2426
      ||| | || | || ||| | |||| | || | || |
```

```
Db      1425
GGCAGCAGGGACAAGTGTTCAGACTGCATGGCCAGCCTAATTGTGGCGAGACAAGGCCT 1484
```

```
Qy      2427
ATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGG 2486
      || || | | ||| | || |||| | | || | |
```

```
Db      1485 ---
TGGGGACATGGCAGTCTCCAACACCATAGGAAGCAACGTGTTTGACATCCTGGTAGG 1541
```

```
Qy      2487 CATCGGCCTGGCCTGGTCCGTGGCCGCCAT 2516
      || | | ||| | || |||
```

```
Db      1542 ACTTGGTGTACCGTGGGGCCTGCAGACCAT 1571
```

```
RESULT 8
US-09-961-679-7
```

```
; Sequence 7, Application US/09961679
; Patent No. 6787352
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: No. 6787352el Human Ion-Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0239-USA
; CURRENT APPLICATION NUMBER: US/09/961,679
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,745
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-961-679-7
```

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Query Match          1.8%; Score 50.8; DB 4; Length 2366;
Best Local Similarity 51.9%; Pred. No. 0.00013;
Matches 140; Conservative 0; Mismatches 127; Indels 3;
Gaps 1;
```

```
Qy      2247
GGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACGCCCATCATTGGGGACCT 2306
      || | ||| | | ||| || | | | | | |||| | |
```

```
Db      1462
GGTCACCTTCATCACGCCACGCTGTGGATCGCTGTGTTCTCCTACATCATGGTGTGGCT 1521
```

```
Qy      2307
GGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGT 2366
      || | | ||| | ||| ||| || | || | | |||
```

```
Db      1522
GGTGACTATTATCGGATACACACTTGGGATCCCGGATGTCATCATGGGCATTACTTTCCT 1581
```

```
Qy      2367
GGCATTGTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGT 2426
      |||| | | || | || |||| | |||| | | || | || |
```

```
Db      1582
GGCAGCAGGGACAAGTGTTCAGACTGCATGGCCAGCCTAATTGTGGCGAGACAAGGCCT 1641
```

```
Qy      2427
ATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAACGCCGTCAATGTCTTCCTGGG 2486
      || ||| | | |||| | || ||||| | | || | |
```

```
Db      1642 ---
TGGGGACATGGCAGTCTCCAACACCATAGGAAGCAACGTGTTTGACATCCTGGTAGG 1698
```

```
Qy      2487 CATCGGCCTGGCCTGGTCCGTGGCCGCCAT 2516
      | | | | | ||| | || ||||
```

```
Db      1699 ACTTGGTGTACCGTGGGGCCTGCAGACCAT 1728
```

RESULT 9



[illegible]

```
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3984 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g181907
US-09-016-434-1199
```

```
Query Match          1.7%; Score 46.2; DB 4; Length 3984;
Best Local Similarity 51.7%; Pred. No. 0.0052;
Matches 105; Conservative 0; Mismatches 98; Indels 0;
Gaps 0;
```

```
Qy          2434
GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
      | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          674
GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 733
```

```
Qy          2494
CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCTG 2553
      | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          734
GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 793
```

```
Qy          2554
GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
      | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          794
CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 853
```

```
Qy          2614 GTGCTCTTGTACCGAAGGCGGCC 2636
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          854 GCCGTCTCCTTCTGGAAGACACC 876
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```
RESULT 11
US-09-799-451-118
; Sequence 118, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
```



```
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 118
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1509)
US-09-799-451-118
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Query Match          1.7%; Score 46.2; DB 4; Length 4473;
Best Local Similarity 51.7%; Pred. No. 0.0057;
Matches 105; Conservative 0; Mismatches 98; Indels 0;
Gaps 0;
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```
Qy          2434
GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          1150
GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 1209
```

```
Qy          2494
CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          1210
GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 1269
```

```
Qy          2554
GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db          1270
CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 1329
```

```
Qy          2614 GTGCTCTTGTACCGAAGGCGGCC 2636
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1330 GCCGTCTCCTTCTGGAAGACACC 1352
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```
RESULT 12
US-09-919-172-61
; Sequence 61, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
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; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 4559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 008942.10
US-09-919-172-61
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Query Match          1.7%; Score 46.2; DB 4; Length 4559;
Best Local Similarity 51.7%; Pred. No. 0.0058;
Matches 105; Conservative 0; Mismatches 98; Indels 0;
Gaps 0;
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```
Qy      2434
GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCATGTCTTCCTGGGCATCGGC 2493
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db      1233
GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 1292
```

```
Qy      2494
CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCTG 2553
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db      1293
GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 1352
```

```
Qy      2554
GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db      1353
CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 1412
```

```
Qy      2614 GTGCTCTTGTACCGAAGCGGCC 2636
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1413 GCCGTCTCCTTCTGGAAGACACC 1435
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# RESULT 13

US-09-701-068-4

```
; Sequence 4, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 4  
; LENGTH: 2803  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-701-068-4

Query Match 1.6%; Score 44.8; DB 4; Length 2803;  
Best Local Similarity 52.1%; Pred. No. 0.011;  
Matches 100; Conservative 0; Mismatches 92; Indels 0;  
Gaps 0;

Qy 477  
GTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536  
||| | | | ||| || ||| || ||| || ||| || |  
||  
Db 950  
GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTTGGCTCAGCTGCATTTGATCTTTT 1009

Qy 537  
CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596  
| |||| | | ||||| ||| || ||||| |||||  
|  
Db 1010  
CCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069

Qy 597  
TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656  
|| | || | | | | ||| | | | || ||||| ||||| ||  
||  
Db 1070  
CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGGGCTTACATCTGGCTATACAT 1129

Qy 657 GATTCTGGCAGT 668  
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Db 1130 AATCCTCGAGGT 1141

RESULT 14  
US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN  
MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 1.6%; Score 44.2; DB 3; Length 4403765;  
Best Local Similarity 46.3%; Pred. No. 4.2;  
Matches 145; Conservative 0; Mismatches 168; Indels 0;  
Gaps 0;

Qy 2213

CCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCA 2272

||| | ||| | ||| ||| ||| ||| ||| |||

|

Db 3929402

CCTCCCTTACCGCCGTTGCCGCCGGCGCCGGCGCCGGCTACGCCGCTGCCGAATCCC 3929343

Qy 2273

TCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTG 2332

| | | ||| || | | ||| | | ||| | |||

|

Db 3929342

GCGCCGCCGCCCTTCGCCGCCGTCCCCACCGTCACCGCCTTGCCGCCGGCGCCGCCCTCG 3929283

Qy 2333

GTCTCAAAGATTCACTCACAGCTGTTGTTTTCTGTCGTCATTGGCACCTCTGTCCCAGATA 2392

||| | | | | | | | | | | | | | | |

|

Db 3929282

CTCGCCACGCCTGTCGTTCCGTTCTGGCCGTCACCACCGCCCCGCCGGTGCCGCCGGTG 3929223

Qy 2393

CGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACG 2452

| | | | | | | | | | | | | | | | |

|

Db 3929222

CCGCCGGCCCCGTTGATGCCGCCGGCGCCGGCGTTGCCGCCGGCCCCGCCCTTGCCGCCCT 3929163

Qy 2453

TGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCG 2512

||| | | | | ||| ||| | | | | | |

||||

Db 3929162

TGGCCGCCGGCGAAGCCGTTGCCGTCTTGGGAGAGGGCGCCGCTGTCGCCGGCCCCGCCG 3929103

Qy 2513 CCATCTACTGGGC 2525

| | | |||

Db 3929102 TCGCCGCCGCGGC 3929090

RESULT 15

US-09-252-991A-9693/c

; Sequence 9693, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9693  
; LENGTH: 1992  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9693

Query Match 1.6%; Score 43.8; DB 4; Length 1992;  
Best Local Similarity 47.5%; Pred. No. 0.017;  
Matches 162; Conservative 0; Mismatches 177; Indels 2;  
Gaps 1;

Qy 2372  
TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431  
|  
Db 738 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--  
GCCGGACGTACCAG 681

Qy 2432  
CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491  
|  
Db 680  
CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 621

Qy 2492  
GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551  
|  
Db 620  
TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCCTGCGCAGCG 561

Qy 2552  
CGGCCGGCACACTGGCCTTCTCCGTCAACCTCTTCACCATCTTTGCATTTGTCTGCATCA 2611  
|  
Db 560  
ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 501

Qy 2612  
GCGTGCTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671  
|  
Db 500  
GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 441

Qy 2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712  
|  
Db 440 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 400

Search completed: January 22, 2005, 17:35:36  
Job time : 241.467 secs

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:25:49 ; Search time 1463.37 Seconds  
(without alignments)  
10860.644 Million cell

updates/sec

Title: US-10-054-680-1  
Perfect score: 2766  
Sequence: 1 atggcgtggttaagggttgca.....gctacatcaaggggttctaa  
2766

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	8 Query Match	Length	DB	ID	Description	
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Appli	2	2766	100.0	3812	13	US-10-054-680-5	Sequence 5,
Appli	3	2761.2	99.8	2782	9	US-09-804-474A-1	Sequence 1,
Appli	4	2733.4	98.8	2781	14	US-10-275-116-1	Sequence 1,
Appli	5	2673.2	96.6	2685	15	US-10-114-153-5	Sequence 5,
Appli	6	2657.6	96.1	2840	15	US-10-114-153-3	Sequence 3,
Appli	7	2367.2	85.6	2813	15	US-10-114-153-1	Sequence 1,
Appli	8	1786.4	64.6	2534	15	US-10-256-537-1	Sequence 1,
Appli	9	1786.4	64.6	2534	15	US-10-256-537-3	Sequence 3,
Appli	10	1784.8	64.5	126512	9	US-09-804-474A-3	Sequence 3,
Appli	11	1784.6	64.5	1863	13	US-10-054-680-3	Sequence 3,
Appli	12	1277	46.2	4282	14	US-10-281-866-1	Sequence 1,
Appli	13	1277	46.2	4282	14	US-10-281-866-3	Sequence 3,
Appli	14	1270.8	45.9	3004	16	US-10-388-934-506	Sequence
506, App	15	1227.8	44.4	4087	9	US-09-901-419-1	Sequence 1,
Appli	16	1208.8	43.7	5438	18	US-10-357-930-24294	Sequence
24294, A	17	1207.2	43.6	6106	16	US-10-062-674-1648	Sequence
1648, Ap	18	897.4	32.4	1187	15	US-10-243-552-809	Sequence
809, App	19	878.4	31.8	2859	18	US-10-723-860-7370	Sequence
c 19	20	821.4	29.7	823	15	US-10-029-386-20265	Sequence
7370, Ap	21	787.2	28.5	1836	9	US-09-864-761-16939	Sequence
20265, A	22	503.4	18.2	505	15	US-10-029-386-6536	Sequence
16939, A	23	494	17.9	551	15	US-10-029-386-4103	Sequence
6536, Ap	24	366	13.2	366	15	US-10-029-386-17804	Sequence
4103, Ap	25	336.4	12.2	507	15	US-10-029-386-4003	Sequence
17804, A	26	219.4	7.9	381	9	US-09-864-761-1172	Sequence
4003, Ap	27	210.2	7.6	502	15	US-10-029-386-7461	Sequence
c 1172, Ap	7461, Ap						

28	208.4	7.5	280	15	US-10-029-386-21161	Sequence
21161, A						
29	186.4	6.7	491	9	US-09-864-761-646	Sequence
646, App						
30	186.2	6.7	276	9	US-09-864-761-17437	Sequence
17437, A						
31	180	6.5	180	15	US-10-029-386-17706	Sequence
17706, A						
32	169	6.1	477	10	US-09-918-995-2005	Sequence
2005, Ap						
33	164.2	5.9	459	9	US-09-864-761-102	Sequence
102, App						
34	146.6	5.3	1132	15	US-10-369-493-30006	Sequence
30006, A						
35	108	3.9	1302	15	US-10-243-552-276	Sequence
276, App						
c 36	95	3.4	151	9	US-09-864-761-17938	Sequence
17938, A						
37	91.4	3.3	1792	15	US-10-369-493-29835	Sequence
29835, A						
38	80.8	2.9	911	18	US-10-425-115-88676	Sequence
88676, A						
39	77.4	2.8	1248	18	US-10-425-115-125495	Sequence
125495,						
40	76.6	2.8	1617	9	US-09-938-842A-2591	Sequence
2591, Ap						
41	76.6	2.8	1617	11	US-09-938-842A-2591	Sequence
2591, Ap						
42	74.2	2.7	611	17	US-10-767-701-15967	Sequence
15967, A						
43	73.4	2.7	968	16	US-10-424-599-94222	Sequence
94222, A						
44	60	2.2	128	9	US-09-864-761-20736	Sequence
20736, A						
c 45	60	2.2	136	15	US-10-029-386-23072	Sequence
23072, A						

#### ALIGNMENTS

##### RESULT 1

US-10-054-680-1

; Sequence 1, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1 Human Ion Exchanger  
Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2766



; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-054-680-1

Query Match 100.0%; Score 2766; DB 13; Length 2766;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2766; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

|||||  
Db 1  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

|||||  
Db 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy 121  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

|||||  
Db 121  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

|||||  
Db 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy 241  
TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

|||||  
Db 241  
TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

|||||  
Db 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy 361  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

|||||  
Db 361  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy 421  
CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

|||||  
Db 421  
CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCT 480

Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

|||||  
Db 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

|||||  
Db 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

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Db 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy 661  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

|||||  
Db 661  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

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Db 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy 781  
ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

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Db 781  
ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy 841  
CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

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Db 841  
CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy 901  
CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

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Db 901  
CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy 961  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020  
|||||  
Db 961  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy 1021  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080  
|||||  
Db 1021  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140  
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Db 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200  
|||||  
Db 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260  
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Db 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320  
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Db 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380  
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Db 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy 1381  
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Db 1381  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy 1441  
TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

|||||  
Db 1441  
TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

|||||  
Db 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

|||||  
Db 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy 1621  
GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

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Db 1621  
GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

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Db 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy 1741  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

|||||  
Db 1741  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

Qy 1801  
AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860

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Db 1801  
AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860

Qy 1861  
CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920

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Db 1861  
CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920

Qy 1921  
GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 1980

|||||  
Db 1921  
GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 1980

Qy 1981  
GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040

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Db 1981  
GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040

Qy 2041  
ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC 2100

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Db 2041  
ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC 2100

Qy 2101  
ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160

|||||  
Db 2101  
ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160

Qy 2161  
TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220

|||||  
Db 2161  
TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220

Qy 2221  
CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280

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Db 2221  
CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280

Qy 2281  
ATGCTCACC GCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2340

|||||  
Db 2281  
ATGCTCACC GCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2340

Qy 2341  
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Db 2341  
GATTCACTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC 2400

Qy 2401  
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Db 2401  
AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460

Qy 2461  
AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520

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Db 2461  
AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520

Qy 2521  
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|||||  
Db 2521  
TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGGCCGGCACACTGGCCTTCTCCGTCACC 2580

Qy 2581  
CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640

|||||  
Db 2581  
CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640

Qy 2641  
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Db 2641  
CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700

Qy 2701  
AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760

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Db 2701  
AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760

Qy 2761 TTCTAA 2766

|||||  
Db 2761 TTCTAA 2766

RESULT 2

US-10-054-680-5

; Sequence 5, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger  
Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 3812

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-054-680-5

Query Match 100.0%; Score 2766; DB 13; Length 3812;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2766; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1  
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Db 618  
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Qy 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

|||||  
Db 678  
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Qy 121  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

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Db 738  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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Db 798  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy 241  
TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

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Db 858  
TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 917

Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db 918  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy 361  
ACCAGCACAACCACTATTGCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

|||||  
Db 978  
ACCAGCACAACCACTATTGCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy 421  
CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

|||||  
Db 1038  
CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540  
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Db 1098  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 1157

Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600  
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Db 1158  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660  
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Db 1218  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy 661  
CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720  
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Db 1278  
CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy 721  
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Db 1338  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy 781  
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Db 1398  
ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy 841  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900  
|||||  
Db 1458  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy 901  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960  
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Db 1518  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy 961  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020  
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Db 1578  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy 1021  
TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

|||||  
Db 1638  
TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

|||||  
Db 1698  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

|||||  
Db 1758  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

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Db 1818  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1877

Qy 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

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Db 1878  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1937

Qy 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

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Db 1938  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy 1381  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

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Db 1998  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy 1441  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

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Db 2058  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy 1501

GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560  
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Db 2118  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620  
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Db 2178  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy 1621  
GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680  
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Db 2238  
GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2297

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740  
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Db 2298  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy 1741  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT 1800  
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Db 2358  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT 2417

Qy 1801  
AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860  
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Db 2418  
AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 2477

Qy 1861  
CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920  
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Db 2478  
CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 2537

Qy 1921  
GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 1980  
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Db 2538  
GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 2597

Qy 1981  
GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG 2040  
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Db 2598

GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG 2657

Qy 2041  
ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTCATGGAGGCCATC 2100

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Db 2658  
ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTCATGGAGGCCATC 2717

Qy 2101  
ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160

|||||  
Db 2718  
ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2777

Qy 2161  
TGCTTTGACTACGTACATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220

|||||  
Db 2778  
TGCTTTGACTACGTACATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2837

Qy 2221  
CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280

|||||  
Db 2838  
CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2897

Qy 2281  
ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2340

|||||  
Db 2898  
ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2957

Qy 2341  
GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC 2400

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Db 2958  
GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC 3017

Qy 2401  
AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460

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Db 3018  
AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 3077

Qy 2461  
AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520

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Db 3078  
AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137

Qy 2521  
TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTCAAC 2580

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Db 3138  
TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 3197

Qy 2581  
CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640

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Db 3198  
CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy 2641  
CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700

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Db 3258  
CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy 2701  
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Db 3318  
AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy 2761 TTCTAA 2766  
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Db 3378 TTCTAA 3383

RESULT 3

US-09-804-474A-1

; Sequence 1, Application US/09804474A  
; Patent No. US20020119518A1  
; GENERAL INFORMATION:  
; APPLICANT: KODET, Stefan et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN  
TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000891  
; CURRENT APPLICATION NUMBER: US/09/804,474A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2782  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-474A-1

Query Match 99.8%; Score 2761.2; DB 9; Length 2782;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2763; Conservative 0; Mismatches 3; Indels 0;  
Gaps 0;

Qy 1  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

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ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTCCTCCATTTTGGGCTGGTTACC 69

Qy 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

|||||  
Db 70  
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Qy 121  
ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

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Db 130  
ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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Db 190  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy 241  
TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

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Db 250  
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Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db 310  
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Qy 361  
ACCAGCACAACTACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

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Db 370  
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Qy 421  
CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480

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Db 430  
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Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

|||||  
Db 490  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 549

Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

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Db 550  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609

Qy 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

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Db 610  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669

Qy 661  
CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

|||||  
Db 670  
CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy 721  
TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

|||||  
Db 730  
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Qy 781  
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Db 790  
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Qy 841  
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Db 850  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy 901  
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Db 910  
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Qy 961  
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Db 970  
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Qy 1021  
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Db 1030  
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Qy 1081  
 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

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 Db 1090  
 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy 1141  
 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

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 Db 1150  
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Qy 1201  
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 Db 1210  
 GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy 1261  
 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

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 Db 1270  
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Qy 1321  
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 Db 1330  
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Qy 1381  
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 Db 1390  
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Qy 1441  
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 Db 1450  
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Qy 1501  
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 Db 1510  
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Qy 1561

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Db 1570  
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Db 1630  
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Qy 1681  
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Db 1690  
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Qy 1741  
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Qy 1861  
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Db 1870  
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Qy 1921  
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Db 1930  
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Db 1990  
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Db 2050



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Qy 2101  
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Db 2110  
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Qy 2161  
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Qy 2221  
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Qy 2281  
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Db 2290  
ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2349

Qy 2341  
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Db 2350  
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Qy 2401  
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Db 2410  
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Qy 2461  
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Db 2470  
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Qy 2521  
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|||||  
Db 2530  
TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGGCACACTGGCCTTCTCCGTCACC 2589

Qy 2581  
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Db 2590  
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Qy 2641  
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Db 2650  
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Qy 2701  
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Db 2710  
AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769

Qy 2761 TTCTAA 2766  
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Db 2770 TTCTAA 2775

RESULT 4  
US-10-275-116-1  
; Sequence 1, Application US/10275116  
; Publication No. US20030096312A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein  
; FILE REFERENCE: HNCX3CWWS  
; CURRENT APPLICATION NUMBER: US/10/275,116  
; CURRENT FILING DATE: 2002-11-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2781  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2781)  
US-10-275-116-1

Query Match 98.8%; Score 2733.4; DB 14; Length 2781;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2762; Conservative 0; Mismatches 1; Indels 18;  
Gaps 1;

Qy 1  
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Qy 61  
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Db 61  
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Qy 121  
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Qy 181  
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Db 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy 241  
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Db 241  
TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTC CATCATTGCTGACCGCTTCATGGCA 300

Qy 301  
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Db 301  
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Qy 361  
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Db 361  
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Qy 421  
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Db 421  
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Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

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Db 481  
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Qy 541  
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Db 541  
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Db 601  
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Qy 661  
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Db 661  
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Db 721  
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Qy 781  
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Db 781  
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Qy 841  
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|||||  
Db 841  
CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy 901  
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Qy 961  
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Db 1141  
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Qy 1261  
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Db 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy 1321  
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Db 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy 1381  
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Db 1381  
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Qy 1441  
TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

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Db 1441  
TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy 1501  
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Db 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy 1561  
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Db 1561  
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Qy 1621  
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Db 1621  
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Qy 1681  
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Db 1681  
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Db 1741  
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Db 1801  
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Qy 1861 CCGAAATGGATGGAACGTGGAATATC-----  
AGATGTGACAGACAGG 1902

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Db 1861  
CCGAAATGGATGGAACGTGGAATATCAGGTGTGAGATTCTTTAAAGATGTGACAGACAGG 1920

Qy 1903  
AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG 1962

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Db 1921  
AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG 1980

Qy 1963  
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Db 1981  
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Qy 2023  
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Db 2041  
GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC 2100

Qy 2083  
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Db 2101  
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Qy 2143  
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Db 2161  
GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG 2220

Qy 2203  
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Db 2221  
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Qy 2263  
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Db 2401  
GTCCCAGATACGTTTGGCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC 2460

Qy 2443  
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Db 2461  
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Qy 2503  
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Db 2521  
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Qy 2563  
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Db 2581  
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Qy 2683

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ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2760

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Db 2761 TATTGCTACATCAAGGGGTTT 2781

# RESULT 5

US-10-114-153-5

; Sequence 5, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Heyes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC  
POLYPEPTIDES, NUCLEIC ACIDS

; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

; FILE REFERENCE: 21402-322A

; CURRENT APPLICATION NUMBER: US/10/114,153

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: 60/281086

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281906



; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282020  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282930  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283512  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283444  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284234  
; PRIOR FILING DATE: 2001-04-17  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 251  
; SEQ ID NO 5  
; LENGTH: 2685  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2685)  
US-10-114-153-5

Query Match 96.6%; Score 2673.2; DB 15; Length 2685;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2675; Conservative 0; Mismatches 3; Indels 0;  
Gaps 0;

Qy 86  
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Qy 146  
CAGGGTCATCGGACTGCAAGGAGGGTGTCTATCTGCCAATCTGGTACCCGGAGAACCCTT 205  
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Db 62  
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Qy 206  
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Qy 266  
TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325  
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Db 182  
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Qy 326  
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Db 242  
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Qy 386  
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Db 302  
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Qy 446  
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Db 362  
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Qy 506  
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Db 422  
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Qy 566  
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Db 482  
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Qy 626  
GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685

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Db 542  
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Qy 686  
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Db 602  
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Qy 746  
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Db 662  
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Qy 806  
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Db 722  
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Qy 866  
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Db 782  
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Qy 926  
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Db 842  
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Qy 986  
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Db 902  
AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 961

Qy 1046  
AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1105

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Db 962  
AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1021

Qy 1106  
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Db 1022  
TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1081

Qy 1166  
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Db 1082  
ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1141

Qy 1226  
AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1285

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Db 1142  
AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1201

Qy 1286  
TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1345

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Db 1202  
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Qy 1346  
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Db 1262  
CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1321

Qy 1406  
TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1465

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Db 1322  
TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1381

Qy 1466  
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Db 1382  
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Qy 1526  
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Db 1442  
CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1501

Qy 1586  
CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1645

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Db 1502  
CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1561

Qy 1646  
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Db 1562  
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Qy 1706  
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Db 1622  
TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681

Qy 1766  
TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG 1825

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Db 1682  
TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG 1741

Qy 1826  
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Db 1742  
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Qy 1886  
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 Db 1802  
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Qy 1946  
 TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATG 2005

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 Db 1862  
 TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATG 1921

Qy 2006  
 AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA 2065

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 Db 1922  
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Qy 2066  
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 Db 1982  
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Qy 2126  
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 Db 2042  
 ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC 2101

Qy 2186  
 TGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCT 2245

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 Db 2102  
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Qy 2246  
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 Db 2162  
 GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC 2221

Qy 2306  
 TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTAGTACAGCTGTTGTTTTTCG 2365

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 Db 2222  
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Qy 2366

TGGCATT TGGCACCTCTGTCCCAGATACGTTT GCCAGCAAAGCTGCTGCCCTCCAGGATG 2425

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Db 2282

TGGCATT TGGCACCTCTGTCCCAGATACGTTT GCCAGCAAAGCTGCTGCCCTCCAGGATG 2341

Qy 2426

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|||||

Db 2342

TATATGCAGACGCCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG 2401

Qy 2486

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Db 2402

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Qy 2546

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Db 2462

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Qy 2606

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Db 2522

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Qy 2666

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Db 2582

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Qy 2726 TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC 2763

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Db 2642 TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC 2679

# RESULT 6

US-10-114-153-3

; Sequence 3, Application US/10114153

; Publication No. US20030185815A1

## ; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

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; APPLICANT: Smithson, Glennda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

```

; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC
POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

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Query Match          96.1%; Score 2657.6; DB 15; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12;
Gaps 1;

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Qy 1  
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Qy 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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Db 123  
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Qy 121  
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Db 183  
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Qy 181  
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Qy 301  
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Db 363  
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Qy 361  
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Db 423  
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Qy 421  
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Db 483  
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Qy 481  
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Db 543  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 602

Qy 541  
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Db 603  
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Qy 601  
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Db 663  
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Qy 661  
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Db 723  
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Qy 721  
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Db 783  
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Qy 781  
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Qy 841  
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Db 903  
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Qy 901  
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Db 963  
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Qy 961  
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Qy 1021  
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Db 1083  
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Qy 1081  
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Db 1143  
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Qy 1141  
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Db 1203  
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Qy 1201  
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Db 1263  
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Qy 1261  
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|||||  
Db 1323  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1382

Qy 1321  
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Db 1383  
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Qy 1381  
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Db 1503  
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Qy 1501  
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|||||

Db 1563  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1622

Qy 1561  
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Db 1623  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy 1621  
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Db 1683  
GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1742

Qy 1681  
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Db 1743  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy 1741  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT 1800  
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Db 1803  
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Qy 1801  
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Db 1863  
AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC 1922

Qy 1861 CCGAAATGGATGGAACGTGGAATATCAGATGTG-----  
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Db 1923  
CCCCGCATGGTGGATATGAGTTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG 1982

Qy 1909  
ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA 1968  
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Db 1983  
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Qy 1969  
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Db 2043  
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Qy 2029  
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Db 2103  
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Qy 2089  
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Db 2163  
ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG 2222

Qy 2149  
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|||||  
Db 2223  
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Qy 2209  
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Db 2283  
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Qy 2269  
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Db 2343  
CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC 2402

Qy 2329  
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|||||  
Db 2403  
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Qy 2389  
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|||||  
Db 2463  
GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC 2522

Qy 2449  
AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG 2508

|||||  
Db 2523  
AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG 2582

Qy 2509  
GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC 2568

|||||  
Db 2583  
GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC 2642

Qy 2569  
TTCTCCGTCACCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA 2628

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Db 2643  
TTCTCCGTCACCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA 2702

Qy 2629  
AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA 2688

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Db 2703  
AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA 2762

Qy 2689  
TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC 2748

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Db 2763  
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Qy 2749 TACATCAAGGGGTTCTAA 2766

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Db 2823 TACATCAAGGGGTTCTAA 2840

RESULT 7

US-10-114-153-1

; Sequence 1, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Mezes, Peter  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Vernet, Corine  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Miller, Charles  
; APPLICANT: Taupier, Raymond J. Jr.  
; APPLICANT: Heyes, Melvyn  
; APPLICANT: Ju, Jingfang  
; APPLICANT: Peyman, John  
; APPLICANT: Catterton, Elina  
; APPLICANT: MacDougall, John  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Stone, David  
; APPLICANT: Mazur, Ann

```

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC
POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2793)
US-10-114-153-1

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Query Match          85.6%; Score 2367.2; DB 15; Length 2813;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2542; Conservative 0; Mismatches 223; Indels 21;
Gaps 2;

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Qy          1
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Db          9
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Qy          61
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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Db          69
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

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Qy          121
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Db 129  
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Qy 181  
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Db 189  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy 241  
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Db 249  
TTTGTGGCCCTGATATACATGTTCCCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db 309  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy 361  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

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Db 369  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy 421  
CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480

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Db 429  
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Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

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Db 489  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 548

Qy 541  
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Db 549  
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Qy 601  
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Db 609  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 668

Qy 661

CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

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Db 669

CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 728

Qy 721

TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

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Db 729

TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 788

Qy 781

ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

|||||

Db 789

ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 848

Qy 841

CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

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Db 849

CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 908

Qy 901

CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

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Db 909

CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 968

Qy 961

AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

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Db 969

AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1028

Qy 1021

TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

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Db 1029

TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1088

Qy 1081

ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC 1140

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Db 1089

ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC 1148

Qy 1141

TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

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Db 1149



TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1208

Qy 1201  
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Db 1209  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1268

Qy 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320  
|||||  
Db 1269  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1328

Qy 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380  
|||||  
Db 1329  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1388

Qy 1381  
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|||||  
Db 1389  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448

Qy 1441  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500  
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Db 1449  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508

Qy 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560  
|||||  
Db 1509  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1568

Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620  
|||||  
Db 1569  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1628

Qy 1621  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680  
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Db 1629  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1688

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

|||||  
Db 1689  
ACAGTCATCGTCCCTTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748

Qy 1741  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT 1800  
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Db 1749  
GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCTCTCAGGTG 1808

Qy 1801  
AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860  
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Db 1809  
AAGATAGTTGATGACGAGGAATATGAGAAAAGGATAATTTCTTCATTGAGCTGGGCCAG 1868

Qy 1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----  
GACAGG 1902  
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Db 1869  
CCCCAGTGGCTTAAGCGAGGGATTTAGCTCTGCTACTCAATCAAGGGGATGGGGACAGG 1928

Qy 1903  
AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG 1962  
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Db 1929  
AAGCTAACAGCCGAGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTTCTT 1988

Qy 1963  
GGTGAACACCCCAAAGTCAAGTCAATGAGAGTCTATGAGTTCAAGACTACGGTG 2022  
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Db 1989  
GGGGAGAACTGCCGGCTGGAGGTCATCATCGAGGAGTCATATGATTTTAAGAACACGGTG 2048

Qy 2023  
GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGAGGGGAC 2082  
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Db 2049  
GATAAACTCATCAAGAAAACGAACTTGGCCTTGGTAATTGGGACCCATTCTTGAGGGGAG 2108

Qy 2083 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAA---  
TCC 2139  
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Db 2109  
CAGTTTTTTAGAGGCAATTACGGTGAGCGCAGGGGACGAGGAGGAGGAGGAGGACGGGTCC 2168

Qy 2140  
GGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACCTCCTGACTGTCTTCTGG 2199  
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Db 2169  
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Qy 2200  
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Db 2229  
AAGGTGCTCTTCGCCTGTGTGCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTTGGT 2288

Qy 2260  
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Db 2289  
GTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCCACTTC 2348

Qy 2320  
GGCTGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCTGTTGGCATTGTCACC 2379  
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Db 2349  
GGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGCACC 2408

Qy 2380  
TCTGTCCCAGATACGTTTGGCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCC 2439  
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Db 2409  
TCCATCCCTGACACGTTGCCAGCAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGACGCG 2468

Qy 2440  
TCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCC 2499  
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Db 2469  
TCCATCGGCAACGTGACCGGCTCCAACGCGGTGAACGTGTTCTTGGCCTGGGCGTCGCC 2528

Qy 2500  
TGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGC 2559  
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Db 2529  
TGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCTTCGAGGTGCGCACTGGC 2588

Qy 2560  
ACACTGGCCTTCTCCGTACCCCTCTTACCATCTTTGCATTTGTCTGCATCAGCGTGCTC 2619  
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Db 2589  
ACGCTGGCCTTCTCCGTACGCTCTTACCGTCTTCGCCTTCGTGGGCATTGCCGTGCTG 2648

Qy 2620  
TTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTC 2679  
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Db 2649  
CTGTACCGGCGCCGGCCGCACATCGGCGGCGAGCTGGGCGGCCCCGCGCGGACCCAAGCTC 2708

Qy 2680  
GCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAG 2739  
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Db 2709  
GCCACCACCGCGCTCTTCCTGGGCCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTGGAG 2768  
  
Qy 2740 GCCTATTGCTACATCAAGGGGTTCTA 2765  
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Db 2769 GCGTACTGCCACATCCGGGGCTTCTA 2794

RESULT 8

US-10-256-537-1  
; Sequence 1, Application US/10256537  
; Publication No. US20030162196A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN  
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER  
; FILE REFERENCE: MPI01-231P1RM  
; CURRENT APPLICATION NUMBER: US/10/256,537  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/325,737  
; PRIOR FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2534  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-256-537-1

Query Match 64.6%; Score 1786.4; DB 15; Length 2534;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1787; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;

Qy 1  
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Db 343  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy 61  
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Db 403  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy 121  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180  
  
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Db 463  
ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240  
  
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Db 523

CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy 241

TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

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Db 583

TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy 301

TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db 643

TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy 361

ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

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Db 703

ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy 421

CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

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Db 763

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Qy 481

ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

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Db 823

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Qy 541

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Db 883

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Qy 601

CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

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Db 943

CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy 661

CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

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Db 1003

CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy 721

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Db 1063  
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Qy 781  
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Db 1123  
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Qy 841  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

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Db 1183  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy 901  
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Db 1243  
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Qy 961  
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Db 1303  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy 1021  
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Db 1363  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

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Db 1423  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

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Db 1483  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

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Db 1543  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy 1261  
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Db 1603  
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Qy 1321  
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Db 1663  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy 1381  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

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Db 1723  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy 1441  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

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Db 1783  
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Qy 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

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Db 1843  
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Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

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Db 1903  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy 1621  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

|||||  
Db 1963  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

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Db 2023  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA 1788

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Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA 2130

RESULT 9

US-10-256-537-3

; Sequence 3, Application US/10256537  
 ; Publication No. US20030162196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carroll, Joseph M.  
 ; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN  
 ; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER  
 ; FILE REFERENCE: MPI01-231P1RM  
 ; CURRENT APPLICATION NUMBER: US/10/256,537  
 ; CURRENT FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: 60/325,737  
 ; PRIOR FILING DATE: 2001-09-28  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2534  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (343)...(2130)

US-10-256-537-3

Query Match 64.6%; Score 1786.4; DB 15; Length 2534;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1787; Conservative 0; Mismatches 1; Indels 0;  
 Gaps 0;

Qy 1

ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

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Db 343

ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy 61

TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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Db 403

TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy 121

ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

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Db 463

ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy 181

CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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Db 523

CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy 241



TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300  
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Db 583  
TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642  
Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360  
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Db 643  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702  
Qy 361  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420  
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Db 703  
ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 762  
Qy 421  
CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480  
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Db 763  
CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822  
Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540  
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Db 823  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 882  
Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600  
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Db 883  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942  
Qy 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660  
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Db 943  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002  
Qy 661  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720  
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Db 1003  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062  
Qy 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780  
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Db 1063

TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy 781  
ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

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Db 1123  
ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy 841  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC 900

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Db 1183  
CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC 1242

Qy 901  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

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Db 1243  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy 961  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

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Db 1303  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy 1021  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

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Db 1363  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC 1140

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Db 1423  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC 1482

Qy 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

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Db 1483  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

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Db 1543  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy 1261  
AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

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Db 1603  
AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

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Db 1663  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy 1381  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

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Db 1723  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy 1441  
TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

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Db 1783  
TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

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Db 1843  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

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Db 1903  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy 1621  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCAGGGT 1680

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Db 1963  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCAGGGT 2022

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

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Db 2023  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA 1788  
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Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA 2130

RESULT 10

US-09-804-474A-3  
 ; Sequence 3, Application US/09804474A  
 ; Patent No. US20020119518A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KODET, Stefan et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN  
 TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: CL000891  
 ; CURRENT APPLICATION NUMBER: US/09/804,474A  
 ; CURRENT FILING DATE: 2001-03-13  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 126512  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(126512)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-804-474A-3

Query Match 64.5%; Score 1784.8; DB 9; Length 126512;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1786; Conservative 0; Mismatches 2; Indels 0;  
 Gaps 0;

Qy 1  
 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

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 Db 2010  
 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy 61  
 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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 Db 2070  
 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy 121  
 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180

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 Db 2130  
 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 2189

Qy 181  
 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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 Db 2190  
 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy 241  
 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

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Db 2250  
TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db 2310  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy 361  
ACCAGCACAAACCATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

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Db 2370  
ACCAGCACAAACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy 421  
CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 480

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Db 2430  
CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 2489

Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

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Db 2490  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 2549

Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

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Db 2550  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

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Db 2610  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy 661  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

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Db 2670  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 2729

Qy 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

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Db 2730  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 2789

Qy 781  
ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840  
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Db 2790  
ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 2849

Qy 841  
CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC 900  
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Db 2850  
CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC 2909

Qy 901  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960  
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Db 2910  
CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 2969

Qy 961  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020  
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Db 2970  
AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 3029

Qy 1021  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080  
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Db 3030  
TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 3089

Qy 1081  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140  
|||||  
Db 3090  
ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 3149

Qy 1141  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200  
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Db 3150  
TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 3209

Qy 1201  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260  
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Db 3210  
GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 3269

Qy 1261  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320  
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Db 3270  
AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 3329

Qy 1321  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

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Db 3330  
AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 3389

Qy 1381  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

|||||  
Db 3390  
CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy 1441  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

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Db 3450  
TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy 1501  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560

|||||  
Db 3510  
GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 3569

Qy 1561  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

|||||  
Db 3570  
GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy 1621  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

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Db 3630  
GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 3689

Qy 1681  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

|||||  
Db 3690  
ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA 1788  
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Db 3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA 3797

RESULT 11  
US-10-054-680-3  
; Sequence 3, Application US/10054680

; Publication No. US20020132998A1  
; GENERAL INFORMATION:  
; APPLICANT: Friddle, Carl Johan  
; APPLICANT: Hilbun, Erin  
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger  
Proteins and Polynucleotides Encoding the  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0301-USA  
; CURRENT APPLICATION NUMBER: US/10/054,680  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/263,384  
; PRIOR FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1863  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-054-680-3

Query Match 64.5%; Score 1784.6; DB 13; Length 1863;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1813; Conservative 0; Mismatches 24; Indels 4;  
Gaps 1;

Qy 1  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

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Db 1  
ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

|||||  
Db 61  
TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy 121  
ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

|||||  
Db 121  
ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

|||||  
Db 181  
CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy 241  
TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300

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Db 241  
TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300



Qy 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360  
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Db 301  
TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy 361  
ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420  
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Db 361  
ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy 421  
CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480  
|||||  
Db 421  
CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540  
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Db 481  
ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

Qy 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600  
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Db 541  
ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy 601  
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|||||  
Db 601  
CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy 661  
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|||||  
Db 661  
CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780  
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Db 721  
TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy 781  
ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840  
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Db 781  
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Qy 841  
 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

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 Db 841  
 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy 901  
 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

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 Db 901  
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Qy 961  
 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

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 Db 961  
 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy 1021  
 TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

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 Db 1021  
 TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy 1081  
 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

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 Db 1081  
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Qy 1141  
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 Db 1141  
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Qy 1201  
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 Db 1201  
 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy 1261  
 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

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 Db 1261  
 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy 1321

Db 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841

US-10-281-866-1

Query Match 46.2%; Score 1277; DB 14; Length 4282;  
Best Local Similarity 69.1%; Pred. No. 0;  
Matches 1843; Conservative 0; Mismatches 775; Indels 51;  
Gaps 5;

Db 208  
AGCACAGGGGGCTGCCAGGGGTCTACCGTGCCAGCCGGGGGTGCTGCTGCCC GTGTGG 267

Db 268  
GAGCCCGACGACCCGTCGCTGGGTGACAAGCGCGGCACGGGCAGTGGTGTACTTTGTGGCC 327

Db 328  
ATGGTCTACATGTTTCTGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAG 387

Db 388  
GTCATCACGTCAAAGAGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTG 447

Db 448  
GGCACCGTTTCGCATCTGGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCC 507

Qy 430  
TCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGT 489  
|||  
Db 508  
TCCGCACCTGAGATCCTGCTGTCTAGTCATCGAAGTCTGCGGCCACAACCTCCAGGCGGGT 567  
Qy 490  
GATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGC 549  
|  
Db 568  
GAGCTGGGCCCAGGCACCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCC 627  
Qy 550  
ATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609  
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Db 628  
GTGTGCATCTACGTATCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTC 687  
Qy 610  
TTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTC 669  
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Db 688  
TTTGTCACTGCCTCTTGGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTT 747  
Qy 670  
TTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCACTCTCTTCTTTCCAGTG 729  
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Db 748  
TTTTCCCCCGGTGTGGTCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTG 807  
Qy 730  
TGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAA 789  
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Db 808  
TGCCTGGTATTTCGCTGGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAG 867  
Qy 790  
AAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAG 849  
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Db 868  
CGCTACCGCACCGACCCACGCAGCGGCATCATCATAGGCGCCGAGGGCGACCCCCGAAG 927  
Qy 850  
GGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAA----- 899  
Db 928  
AGCATCGAGCTGGACGGCACGTTCGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTG 987  
Qy 900 --  
CTGGTGCCCTGGAAGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATT 957  
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Db          988
GGCCCGGGCCCCGCCGAGGCGCGCAGCTGGACGCCAGCCGCCGCGAGGTTCATCCAGATC 1047

Qy          958
CTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCC 1017
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Db          1048
CTCAAGGACCTCAAGCAGAAGCACCCGGACAAGGATCTGGAGCAGCTGGTGGGCATCGCC 1107

Qy          1018
AATTACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACT 1077
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Db          1108
AACTACTACGCGCTGCTGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACG 1167

Qy          1078
CGTATGATGACTGGTGCAAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAG 1137
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|
Db          1168
CGGCTGATGACCGGCGCCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGG 1227

Qy          1138
GCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTC 1197
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Db          1228 GCGGC---
GCCGCGCGAGGGCGCGGGCGAGGACGAAGACGACGGGCGCCAGCCGCATCTTC 1284

Qy          1198
TTTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTG 1257
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|
Db          1285
TTCGAGCCTAGCCTCTACCACTGCCTGGAGAACTGCGGCTCCGTGCTGCTGTCCGTCACG 1344

Qy          1258
AGGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCT 1317
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Db          1345
TGCCAGGGCGGCGAGGGCAACAGCACCTTCTACGTGGACTACCGCACTGAGGACGGCTCT 1404

Qy          1318
GCCAATGCAGGGGCTGACTATGAGTTACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAG 1377
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Db          1405
GCCAAGGCGGGCTCCGACTACGAGTACAGCGAGGGGCACGCTGGTGTTCAAACCAGGCGAG 1464

Qy          1378
ACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACAC 1437
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Db          1465
ACGCAGAAGGAGCTGCGCATCGGCATCATCGACGACGACATCTTCGAGGAGGACGAGCAT 1524

Qy          1438

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TTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCT 1497  
 Db 1525  
 TTCTTCGTGCGGCTGCTGAACCTGCGCGTGGGCGACGCGCAGGGCATGTTTCGAGCCG--- 1581  
 Qy 1498  
 CCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCC 1557  
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 Db 1582 -----  
 GACGGCGGGCGGGCGGGCCCAAGGGCGGGCTGGTGGCGCCGCTGCTGGCC 1629  
 Qy 1558  
 ACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT 1617  
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 Db 1630  
 ACCGTCAACATCCTGGACGACGACCACGCAGGCATCTTCTCCTTCCAGGACCGCTGCTG 1689  
 Qy 1618  
 CATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCG 1677  
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 Db 1690  
 CACGTGAGCGAGTGCATGGGCACCGTGGACGTGCGCGTCGTGCGCAGCTCGGGCGCGCGC 1749  
 Qy 1678  
 GGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC 1737  
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 Db 1750  
 GGCACCGTGCGCCTTCCCTACCGCACGGTGGACGGCACGGCGCGCGGGCGGGCGGTGCAC 1809  
 Qy 1738  
 TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGG 1797  
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 Db 1810  
 TACGAGGACGCGTGCGGAGAGCTGGAGTTTGGCGACGACGAGACCATGAAACTCTTCAG 1869  
 Qy 1798  
 GTTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT 1857  
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 Db 1870  
 GTGAAGATAGTTGATGACGAGGAATATGAGAAAAGGATAATTTCTTCATTGAGCTGGGC 1929  
 Qy 1858 GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----  
 GAC 1899  
 |||  
 Db 1930  
 CAGCCCCAGTGGCTTAAGCGAGGGATTTTCAGCTCTGCTACTCAATCAAGGGGATGGGGAC 1989  
 Qy 1900  
 AGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTA 1959  
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 Db 1990  
 AGGAAGCTAACAGCCGAGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTT 2049

Qy 1960  
TTGGGTGAACACCCCAAAGTAGAAGTCATCATTTGAGAGTCTATGAGTTCAAGACTACG 2019  
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Db 2050  
CTTGGGGGAGAACTGCCCGCTGGAGGTCATCATCGAGGAGTCATATGATTTTAAGAACACG 2109

Qy 2020  
GTGGACAAGCTGATCAAGAAGACAAACCTGGCCTTGTTTGGGGGACCCATTCTGGAGG 2079  
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Db 2110  
GTGGATAAACTCATCAAGAAAACGAACTTGGCCTTGTTAATTGGGACCCATTCATGGAGG 2169

Qy 2080 GACCAGTTCATGGAGGCCATCACCGTCAGTGCAGC---  
AGGGGATGAGGATGAGGATGAA 2136  
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Db 2170  
GAGCAGTTTTTAGAGGCAATTACGGTGAGCGCAGGGGACGAGGAGGAGGAGGAGGACGGG 2229

Qy 2137  
TCCGGGGAGGAGAGGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTC 2196  
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Db 2230  
TCCCAGGAGGAGCGGGCTGCCGTCGTGCTTTGACTACGTGATGCACTTCCTGACGGTGTTTC 2289

Qy 2197  
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Db 2290  
TGGAAGGTGCTCTTCGCCTGTGTGCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTT 2349

Qy 2257  
GCCGTCTCCATCCTCATCTTGGCATGCTCACCGCCATCATTTGGGGACCTGGCCTCGCAC 2316  
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Db 2350  
GGTGTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTTGGGGACCTCGCCTCCCAC 2409

Qy 2317  
TTCGGCTGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTGTC 2376  
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Db 2410  
TTCGGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGC 2469

Qy 2377  
ACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGAC 2436  
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Db 2470  
ACCTCCATCCCTGACACGTTTCGCCAGCAAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGAC 2529

Qy 2437  
GCCTCCATTGGCAACGTGACGGGAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTG 2496  
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Query Match 46.2%; Score 1277; DB 14; Length 4282;  
Best Local Similarity 69.1%; Pred. No. 0;  
Matches 1843; Conservative 0; Mismatches 775; Indels 51;  
Gaps 5;

Qy 130  
AACAAATGAGTCCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTGCCAATCTGG 189  
| | | | | | | | | | | | | | | | | | | | | |

Db 208  
AGCACAGGGGGCTGCCAGGGGTCTACCGCTGCCAGCCGGGGGTGCTGCTGCCCCGTGTGG 267

Qy 190  
TACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCC 249  
| | | | | | | | | | | | | | | | | | | | | |

Db 268  
GAGCCCGACGACCCGTCGCTGGGTGACAAGGCGGCACGGGCAGTGGTGTACTTTGTGGCC 327

Qy 250  
CTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAA 309  
| | | | | | | | | | | | | | | | | | | | | |

Db 328  
ATGGTCTACATGTTTCTGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAG 387

Qy 310  
GTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACA 369  
| | | | | | | | | | | | | | | | | | | | | |

Db 388  
GTCATCACGTCAAAAGAGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTG 447

Qy 370  
ACCACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTC 429  
| | | | | | | | | | | | | | | | | | | | | |

Db 448  
GGCACCGTTCGCATCTGGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCC 507

Qy 430  
TCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGT 489  
| | | | | | | | | | | | | | | | | | | | | |

Db 508  
TCCGCACCTGAGATCCTGCTGTCAAGTCTGCGGCCACAACCTCCAGGCGGGT 567

Qy 490  
GATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGC 549  
| | | | | | | | | | | | | | | | | | | | | |

Db 568  
GAGCTGGGCCCAGGCACCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCC 627

Qy 550  
ATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609  
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Db 628  
GTGTGCATCTACGTACATCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTC 687

Qy 610  
 TTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTC 669  
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 Db 688  
 TTTGTCACTGCCTCTTGGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTT 747  
  
 Qy 670  
 TTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTG 729  
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 Db 748  
 TTTTCCCCCGGTGTGGTCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTG 807  
  
 Qy 730  
 TGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAA 789  
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 Db 808  
 TGCGTGGTATTGCGCTGGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAG 867  
  
 Qy 790  
 AAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAG 849  
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 Db 868  
 CGCTACCGCACCGACCCACGCAGCGGCATCATCATAGGCGCCGAGGGCGACCCCCGAAG 927  
  
 Qy 850  
 GGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAA----- 899  
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 Db 928  
 AGCATCGAGCTGGACGGCACGTTTCGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTG 987  
  
 Qy 900 --  
 CCTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATT 957  
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 Db 988  
 GGCCCGGGCCCCGCCGAGGCGCGCGAGCTGGACGCCAGCCGCCGCGAGGTCATCCAGATC 1047  
  
 Qy 958  
 CTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCC 1017  
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 Db 1048  
 CTCAAGGACCTCAAGCAGAAGCACCCGGACAAGGATCTGGAGCAGCTGGTGGGCATCGCC 1107  
  
 Qy 1018  
 AATTACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACT 1077  
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 Db 1108  
 AACTACTACGCGCTGCTGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACG 1167  
  
 Qy 1078  
 CGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAG 1137  
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Db 1168  
 CGGCTGATGACCGGCGCCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGG 1227

Qy 1138  
 GCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTC 1197  
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Db 1228 GCGGC---  
 GCCGGCCGAGGGCGCGGGCGAGGACGAAGACGACGGCGCCAGCCGCATCTTC 1284

Qy 1198  
 TTTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTG 1257  
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Db 1285  
 TTCGAGCCTAGCCTCTACCACTGCCTGGAGAACTGCGGCTCCGTGCTGCTGTCCGTCACG 1344

Qy 1258  
 AGGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCT 1317  
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Db 1345  
 TGCCAGGGCGGCGAGGGCAACAGCACCTTCTACGTGGACTACCGCACTGAGGACGGCTCT 1404

Qy 1318  
 GCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAG 1377  
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Db 1405  
 GCCAAGGCGGGCTCCGACTACGAGTACAGCGAGGGCACGCTGGTGTTCAAACCAGGCGAG 1464

Qy 1378  
 ACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTTGAGGAGGATGAACAC 1437  
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Db 1465  
 ACGCAGAAGGAGCTGCGCATCGGCATCATCGACGACGACATCTTCGAGGAGGACGAGCAT 1524

Qy 1438  
 TTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCT 1497  
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Db 1525  
 TTCTTCGTGCGGCTGCTGAACCTGCGCGTGGGCGACGCGCAGGGCATGTTTCGAGCCG--- 1581

Qy 1498  
 CCAGCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCC 1557  
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Db 1582 -----  
 GACGGCGGCGGGCGGCCCAAGGGGCGGCTGGTGGCGCCGCTGCTGGCC 1629

Qy 1558  
 ACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT 1617  
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Db 1630  
 ACCGTCAACATCCTGGACGACGACCACGCAGGCATCTTCTCCTTCAGGACCGCCTGCTG 1689

Qy 1618  
 CATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGG 1677

||  
Db 1690  
CACGTGAGCGAGTGCATGGGCACCGTGGACGTGCGCGTCGTGCGCAGCTCGGGCGCGCGC 1749  
Qy 1678  
GGTACAGTCATCGTCCCCCTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC 1737  
||  
Db 1750  
GGCACCGTGCGCCTTCCCTACCGCACGGTGGACGGCACGGCGCGCGGGCGGGCGGTGCAC 1809  
Qy 1738  
TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAAG 1797  
|  
Db 1810  
TACGAGGACGCGTGC GGAGAGCTGGAGTTTGGCGACGACGAGACCATGAAAACCTCTTCAG 1869  
Qy 1798  
GTTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT 1857  
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Db 1870  
GTGAAGATAGTTGATGACGAGGAATATGAGAAAAAGGATAATTTCTTCATTGAGCTGGGC 1929  
Qy 1858 GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----  
GAC 1899  
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Db 1930  
CAGCCCCAGTGGCTTAAGCGAGGGATTTTCAGCTCTGCTACTCAATCAAGGGGATGGGGAC 1989  
Qy 1900  
AGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTA 1959  
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Db 1990  
AGGAAGCTAACAGCCGAGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTT 2049  
Qy 1960  
TTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACG 2019  
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Db 2050  
CTTGGGGAGAACTGCCGGCTGGAGGTCATCATCGAGGAGTCATATGATTTTAAGAACACG 2109  
Qy 2020  
GTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGAGG 2079  
|||  
Db 2110  
GTGGATAAACTCATCAAGAAAACGAACTTGGCCTTGGTAATTGGGACCCATTTCATGGAGG 2169  
Qy 2080 GACCAGTTCATGGAGGCCATCACCGTCAGTGCAGC---  
AGGGGATGAGGATGAGGATGAA 2136  
Db 2170  
GAGCAGTTTTTTAGAGGCAATTACGGTGAGCGCAGGGGACGAGGAGGAGGAGGAGGACGGG 2229

Qy 2137  
TCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTACATGCACCTTCCTGACTGTCTTC 2196  
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|||  
Db 2230  
TCCCAGGAGGAGCGGCTGCCGTCGTGCTTTGACTACGTGATGCACCTTCCTGACGGTGTTTC 2289

Qy 2197  
TGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTC 2256  
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Db 2290  
TGGAAGGTGCTCTTCGCCTGTGTGCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTT 2349

Qy 2257  
GCCGCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCAC 2316  
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Db 2350  
GGTGTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCAC 2409

Qy 2317  
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Db 2410  
TTCGGCTGCACCATTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGC 2469

Qy 2377  
ACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGAC 2436  
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Db 2470  
ACCTCCATCCCTGACACGTTTCGCCAGCAAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGAC 2529

Qy 2437  
GCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTGCGCATCGGCCTG 2496  
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|  
Db 2530  
GCGTCCATCGGCAACGTGACCGGCTCCAACGCCGTGAACGTGTTCTTGGCCTGGGCGTC 2589

Qy 2497  
GCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGGCC 2556  
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|  
Db 2590  
GCCTGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCTTCGAGGTGCGCACT 2649

Qy 2557  
GGCACACTGGCCTTCTCCGTACCCCTCTTACCATCTTTGCATTTGTCTGCATCAGCGTG 2616  
||| ||||||| ||||||| ||||||| |||| || || || |||||  
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Db 2650  
GGCACGCTGGCCTTCTCCGTACGCTCTTACCCTCTTCGCCTTCGTGGGCATTGCCGTG 2709

Qy 2617  
CTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAG 2676  
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Db 246  
GTTCTTGGGTCTGTCTATCATTGCTGATCGTTTTATGGCATCCATTGAGGTCATCACATC 305

Qy 321  
TCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAAACCACTATTTCG 380  
| ||| || | | | | | |||| | |||| |

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Db 306  
CAAGGAGAAAGAGATCACCATCACCAAGGCAAATGGGGAGACCAGCGTGGGCACTGTACG 365

Qy 381  
GGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGA 440  
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Db 366  
CATCTGGAATGAAACGGTGTCCAACCTTACACTCATGGCCCTGGGCTCCTCAGCACCTGA 425

Qy 441  
GATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTATTGCTGGTGATCTGGGACC 500  
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Db 426  
GATTCTGCTGTCTGTCTCATCGAGGTCTGTGGCCACAACCTTCCAGGCGGGTGAGCTAGGCC 485

Qy 501  
TTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTA 560  
| |||| | | | |||| | ||||||||| | | |||| | | |||| |

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Db 486  
AGGCACCATCGTGGGCAGTGCCGCCTTCAACATGTTTGTGGTCATTGCTGTGTGTGTGTA 545

Qy 561  
CGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGC 620  
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Db 546  
TGTCATCCCGGCTGGTGAGAGCCGTAAGATCAAGCACTTAAGGGTCTTCTTCGTACACAGC 605

Qy 621  
TGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCCTGG 680  
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Db 606  
CTCTTGGAGCATCTTTGCCTATGTCTGGCTTTATCTCATTTCTAGCAGTTTTCTCTCCAGG 665

Qy 681  
TGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCT 740  
| ||||||||| |||| | | |||| | | |||||| | | |||||| |

|  
Db 666  
CGTGGTCCAGGTGTGGGAGGCACTGCTCACGCTGGTCTTCTTCCCGGTGTGTGTGGTGTT 725

Qy 741  
GGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCAC 800  
| |||| | || | | | ||||||||| |||| | |||| | |

|||||  
Db 726  
CGCCTGGATGGCGGACAAGCGACTGCTCTTCTACAAGTACGTGTACAAGCGCTATCGCAC 785



Qy 801 AGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGAT 860  
|  
Db 786 CGACCCTCGCAGCGGAATCATCATCGGGGCAGAGGGAGACCCGCCCCAAGAGCATCGAGCT 845  
Qy 861 GGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAA-----  
CCTGGTGCC 908  
|  
|  
Db 846 GGATGGCACATTCTGTGGGCACTGAGGTCCCAGGCGAGCTGGGTGCATTGGGCACAGGTCC 905  
Qy 909 CCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCT 968  
|  
|  
Db 906 CGCTGAGGCGCGTGAGCTGGACGCCAGCCGGCGCGAGGTCATCCAGATTCTTAAGGACTT 965  
Qy 969 GAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGC 1028  
|  
|  
Db 966 AAAGCAGAAGCACCCGGATAAGGACCTGGAGCAGCTGGTGGGCATCGCCAAGTACTATGC 1025  
Qy 1029 TCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGAC 1088  
|  
|  
Db 1026 ACTGCTGCACCAGCAGAAGAGCCGTGCCTTCTACCGCATCCAGGCCACGCGGCTGATGAC 1085  
Qy 1089 TGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCAT 1148  
|  
Db 1086 AGGTGCGGGCAACGTGCTGCGCCGACACGCTGCGGATGCTGCCCCGAGG--  
CCTGGGGC 1142  
Qy 1149 GAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATG 1208  
|  
|  
Db 1143 CAACGATGGTGGCCCCGATGATGAGGACGATGGTGCCAGCCGCATCTTCTTTGAGCCCAG 1202  
Qy 1209 TTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGG 1268  
|  
|  
Db 1203 CCTCTACCACTGCCTGGAGAACTGCGGGTCAGTGCTGCTGTCGGTGGCTTGCCAGGGTGG 1262  
Qy 1269 AGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGG 1328  
|  
|

[illegible]

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Db          1788
GGACGACGAAGAGTATGAGAAGAAGGACAACCTTCTTCATCGAGCTGGGCCAGCCCCAGTG 1847

Qy          1869 GATGGAACGTGGAATATCAGATGTGAC-----
AGACAGGAAGCTGAC 1910
      | | | | | | | | | | | | | |
|||||||
Db          1848
GCTTAAGCGGGGCATCTCAGCTCTGCTACTCAACCAAGGGGATGGAGACAGGAAGCTGAC 1907

Qy          1911
TATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACA 1970
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|
Db          1908
TGCAGAGGAGGAGGAGGCCAGAGGATAGCAGAGATGGGCAAGCCAGTTCTTGGGGAGAA 1967

Qy          1971
CCCCAACTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACT 2030
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|||||
Db          1968
CTGTCGCCTCGAGGTCATCATCGAGGAGTCTTATGACTTTAAGAATACGGTGGATAAACT 2027

Qy          2031
GATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCAT 2090
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|
Db          2028
CATAAAGAAAACAAACCTGGCCTTGGTGATTGGGACCCACTCATGGAGGGAGCAGTTTTT 2087

Qy          2091 GGAGGCCATCACCGTCAGTGCAGCA---
GGGGATGAGGATGAGGATGAATCCGGGGAGGA 2147
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|||||
Db          2088
AGAGGCAGTTACAGTGAGCGCAGGGGACGAGGAGGAGGATGAGGATGGGTCTCGTGAGGA 2147

Qy          2148
GAGGCTGCCCTCCTGCTTTGACTACGTGATGCACTTCTGACTGTCTTCTGGAAGGTGCT 2207
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
||
Db          2148
GCGGCTGCCATCCTGCTTTGACTACGTGATGCACTTCTGACGGTGTTCTGGAAAGTTCT 2207

Qy          2208
GTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCAT 2267
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|||
Db          2208
GTTTCGCCTGCCTTCCACCCACGGAGTACTGCCATGGCTGGGCCTGCTTTGGTGTCTGCAT 2267

Qy          2268
CCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCAC 2327
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|||||
Db          2268
CCTGGTCAATTGGTCTGCTCACTGCCCTCATCGGAGACCTGGCCTCACACTTTGGGTGCAC 2327

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; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF
RECOMBINANT
; TITLE OF INVENTION:  PROTEINS
; FILE REFERENCE:  UMO1531.1
; CURRENT APPLICATION NUMBER:  US/09/901,419
; CURRENT FILING DATE:  2001-07-09
; PRIOR APPLICATION NUMBER:  60/218,125
; PRIOR FILING DATE:  2000-01-13
; NUMBER OF SEQ ID NOS:  2
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH:  4087
; TYPE:  DNA
; ORGANISM:  Bos taurus
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  (268)..(3180)
; NAME/KEY:  sig_peptide
; LOCATION:  (268)..(363)
; NAME/KEY:  misc_feature
; LOCATION:  (3178)
; OTHER INFORMATION:  A Poly (H) affinity tag comprising 6 His residues
; OTHER INFORMATION:  have been inserted at the C-Terminus end of the
; OTHER INFORMATION:  coding region of the protein
US-09-901-419-1
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Query Match          44.4%;  Score 1227.8;  DB 9;  Length 4087;
Best Local Similarity  67.1%;  Pred. No. 0;
Matches 1935;  Conservative    0;  Mismatches  777;  Indels  171;
Gaps      7;
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Qy          46
TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
      |||  || | || | |||  || || |  | |  |  |||
Db          307
TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366
```

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Qy          106
GGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAG 165
      ||  || | |  ||| | | ||  ||| | || | |||
|||
Db          367
ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426
```

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Qy          166
GAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCTTCCCTTGGGGACAAGATTGCC 225
      |||| | | | | | | | | | | | | | | | | | | | |
|||||
Db          427
AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486
```

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Qy          226
AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT 285
      || | | ||| ||||| || | ||||| |||| | |
|||||||
Db          487
AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGAGTCTCAATCATTGCT 546
```

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Qy          286
GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
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|||  
 Db 547  
 GACCGGTTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606

Qy 346  
 AAACCCAATGGAGAAACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAAC 405  
 |||||

Db 607  
 AAACCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAGACAGTGTCCAAC 666

Qy 406  
 CTGACCCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465  
 |||||

Db 667  
 CTGACCTTGATGGCCCTGGGGTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG 726

Qy 466  
 TGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCC 525  
 ||

Db 727  
 TGTGGCCATAACTTCACTGCAGGAGACCTTGGCCCTAGCACCATCGTGGGGAGTGCTGCA 786

Qy 526  
 TTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGC 585  
 |

Db 787  
 TTCAACATGTTTCATCATCATTTGCCCTTTGTGTGTATGTCGTCCCGGATGGGGAGACAAGG 846

Qy 586  
 AAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATC 645  
 |

Db 847  
 AAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCATGGAGCATCTTTGCCTATACC 906

Qy 646  
 TGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTC 705  
 |

Db 907  
 TGGCTTTACATCATTTTGTCTGTCTCAGCTCCCCTGGGGTCTGGAGGTCTGGGAAGGTTTG 966

Qy 706  
 CTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTG 765  
 ||

Db 967  
 CTTACTTTCTTCTTCTTCCCCTATCTGCGTTGTGTTTGCTTGGGTGGCAGACAGGAGGCTT 1026

Qy 766  
 CTCTTCTACAAATACATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA 825  
 ||

Db 1027  
 CTGTTTTACAAGTATGTCTACAAGAGGTATCGGGCTGGCAAGCAGAGGGGAATGATTATT 1086

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Qy      826 GAGACAGAGGGTGACCACC-----
TAAGGGCATTGAGATGGATGGGAAAATGATG 876
      ||      || || || ||      |      |      |||| |||| |||| |||| ||
|
Db      1087
GAACACGAAGGAGACAGGCCATCTTCCAAGACAGAAATTGAAATGGATGGGAAAGTGGTC 1146

Qy      877 AATTCCCATTTTTC-----
TAGATGGGAACCTGGTGCCCTGGAAGGGAAG----- 921
      |||| || ||      |||| ||      |||| |      || |      ||
Db      1147
AATTCCCATGTTGACAGTTTCTTAGATGGAGCCCTGGTTCTGGAGTTGATGAGAGGGAC 1206

Qy      922 ---
GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA 978
      || |      || || || || |      |||| ||      |||| || || || ||
||
Db      1207
CAAGATGATGAAGAAGCCAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTCAAGCAGAAG 1266

Qy      979
CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCAC 1038
      || |||| |||| || || || |      | || |      |||| || || || ||
||
Db      1267
CATCCAGAGAAGGAAATAGAGCAATTAATAGAATTAGCCAATTACCAAGTCTTAAGTCAG 1326

Qy      1039
CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC 1098
      || || || || || || || || |||| || || || || || || || || ||
|||||
Db      1327
CAGCAAAAAGTCGAGCGTTTTACCGTATTCAAGCTACCCGCCTGATGACCGGAGCAGGC 1386

Qy      1099
AATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTG 1158
      || || |      |||| |||| |||| || || || || || || || || ||
|||||
Db      1387
AACATTTTAAAGAGGCATGCAGCAGACCAAGCCAGGAAAGCTGTCAGCATGCATGAGGTC 1446

Qy      1159 CACACCGATGAGCCTG---
AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
      |||| || |      || || || || || || || || || || || || || ||
||
Db      1447
AACACGGAAGTGGCTGAAAATGACCCTGTCAGTAAGATCTTCTTTGAACAAGGGACATAT 1506

Qy      1216
CAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATG 1275
      |||| |||| |||| || || || || || || || || || || || || || ||
||
Db      1507
CAGTGTCTGGAGAAGTGTGGCACAGTAGCCCTGACCATTATCCGCAGAGGTGGTGATTG 1566

Qy      1276
TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
      | || || || || || || || || || || || || || || || || || ||
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[illegible]



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Db          2098      ||||| | | | | | | | | | | | | | | | | | | |
GAGGAGTATGAGAAAAACAAGACCTTCTTCCTTGAGATTGGAGAGCCCCGCCTGGTGGAG 2157

Qy          1874 -----
AACGTGGAA 1882

||
Db          2158
ATGAGTGAGAAGAAAGCCCTGTTATTGAATGAGCTTGGTGGCTTCACAATAACAGGGAAA 2217

Qy          1883
TATCAGATGTGACAGACAG----- 1901
        || | |   | ||| | |

Db          2218
TACCTGTATGGCCAGCCTGTCTTCAGGAAAGTTCATGCTAGAGAACATCCACTCCCCTCT 2277

Qy          1902 -----
GAAGCTGACTATGGAAGAAGAG 1923
                                | | |||| | ||||

|||
Db          2278
ACTATAATCACCATCGCAGATGAATATGATGACAAGCAGCCACTGACCAGCAAAGAGGAG 2337

Qy          1924
GAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAACTAGAA 1983
        || | | | | | | | | | | | | | | | | | | | | | | | | | |

||
Db          2338
GAAGAGAGGCGCATTCGCGAAATGGGGCGCCCCATTCTGGGAGAGCACACCAGACTGGAG 2397

Qy          1984
GTCATCATTTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACA 2043
        || ||||||||| |||| ||||||||| || ||||||||| ||||

|||||||
Db          2398
GTGATCATTTGAAGAATCCTACGAGTTCAAGAGTACCGTGGACAAACTGATTAAGAAGACA 2457

Qy          2044
AACCTGGCCTTGTTGTGGGGACCCATTCTTGAGGGGACCAGTTCATGGAGGCCATCACC 2103
        ||||| ||| | || || ||||| | | ||||| || ||||||| |||||

|||||
Db          2458
AACCTAGCCCCTCGTGGTTGGGACGAACAGCTGGAGAGAGCAGTTCATCGAGGCGATCACT 2517

Qy          2104
GTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGC 2163
        ||||||| | | ||||| |||| | |||| |||||||||

|||||||
Db          2518
GTCAGTGCTGGGGAAGATGACGATGACGACGAATGTGGGGAGGAGAAGCTGCCCTCCTGT 2577

Qy          2164
TTTGACTACGTCATGCACCTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCC 2223
        ||||||||| ||||||| ||||||| ||||||||| || || ||||| |||

|||
Db          2578
TTTGACTACGTGATGCACCTTCTGACTGTGTTCTGGAAGGTCCTCTTCGCCTTTGTCCCC 2637

Qy          2224

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CCCACAGAGTACTGCCACGGCTGGGCGCTGCTTCGCCGTCTCCATCCTCATTCATTGGCATG 2283  
|  
Db 2638  
CCGACAGAGTACTGGAACGGCTGGGCGTGTTCATCGTCTCCATCCTCATGATCGGCCTA 2697  
Qy 2284  
CTCACCGCCATCATTTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGAT 2343  
|||  
Db 2698  
CTGACGGCTTTCATTGGAGACCTCGCTTCCCCTTCGCCTGCACCATCGCCCTGAAGGAT 2757  
Qy 2344  
TCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCAGATACGTTTGCCAGC 2403  
|||  
Db 2758  
TCCGTGACCGCGGTGGTGTTCGTTGCGCTTGGAACCTCAGTGCCAGACACATTTGCAAGC 2817  
Qy 2404  
AAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGC 2463  
|||  
Db 2818  
AAAGTGGCCGCCACCCAGGACCAGTATGCGGATGCATCCATAGGTAACGTACAGGCAGC 2877  
Qy 2464  
AACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGG 2523  
Db 2878  
AACGCGGTGAACGTCTTCCTGGGCATCGGTGTGGCCTGGTCCATCGCCGCCATCTACCAC 2937  
Qy 2524  
GCTCTGCAGGGACAGGAGTTCACAGTGTGCGCCGGCACACTGGCCTTCTCCGTCAACCTC 2583  
|||  
Db 2938  
GCGGCCAACGGGGAACAGTTCAAAGTGTCCCCTGGCACGCTAGCTTTTTCTGTCACTCTC 2997  
Qy 2584  
TTCACCATCTTTGCATTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTG 2643  
|  
Db 2998  
TTCACCATTTTTGCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGGCCAGAAATT 3057  
Qy 2644  
GGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGC 2703  
|  
Db 3058  
GGAGGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTCTTTGTGCTC 3117  
Qy 2704  
CTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC 2763  
|||  
Db 3118  
CTGTGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAAGGCTTC 3177

Qy 2764 TAA 2766  
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Db 3178 TAA 3180

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Job time : 1477.37 secs